

FIG. 1A

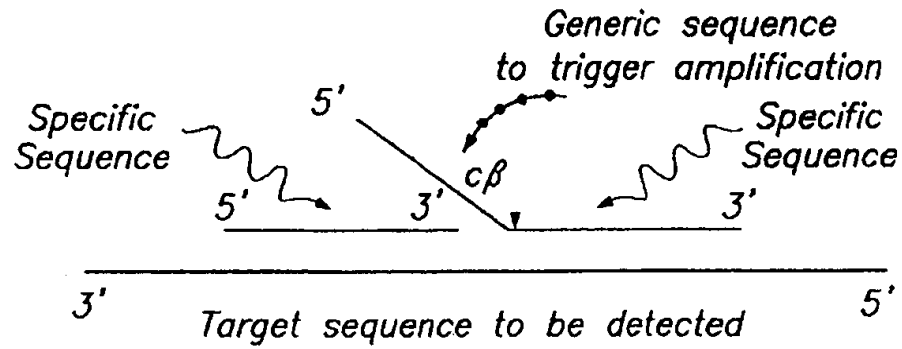


FIG. 1B PART ONE: TRIGGER REACTION

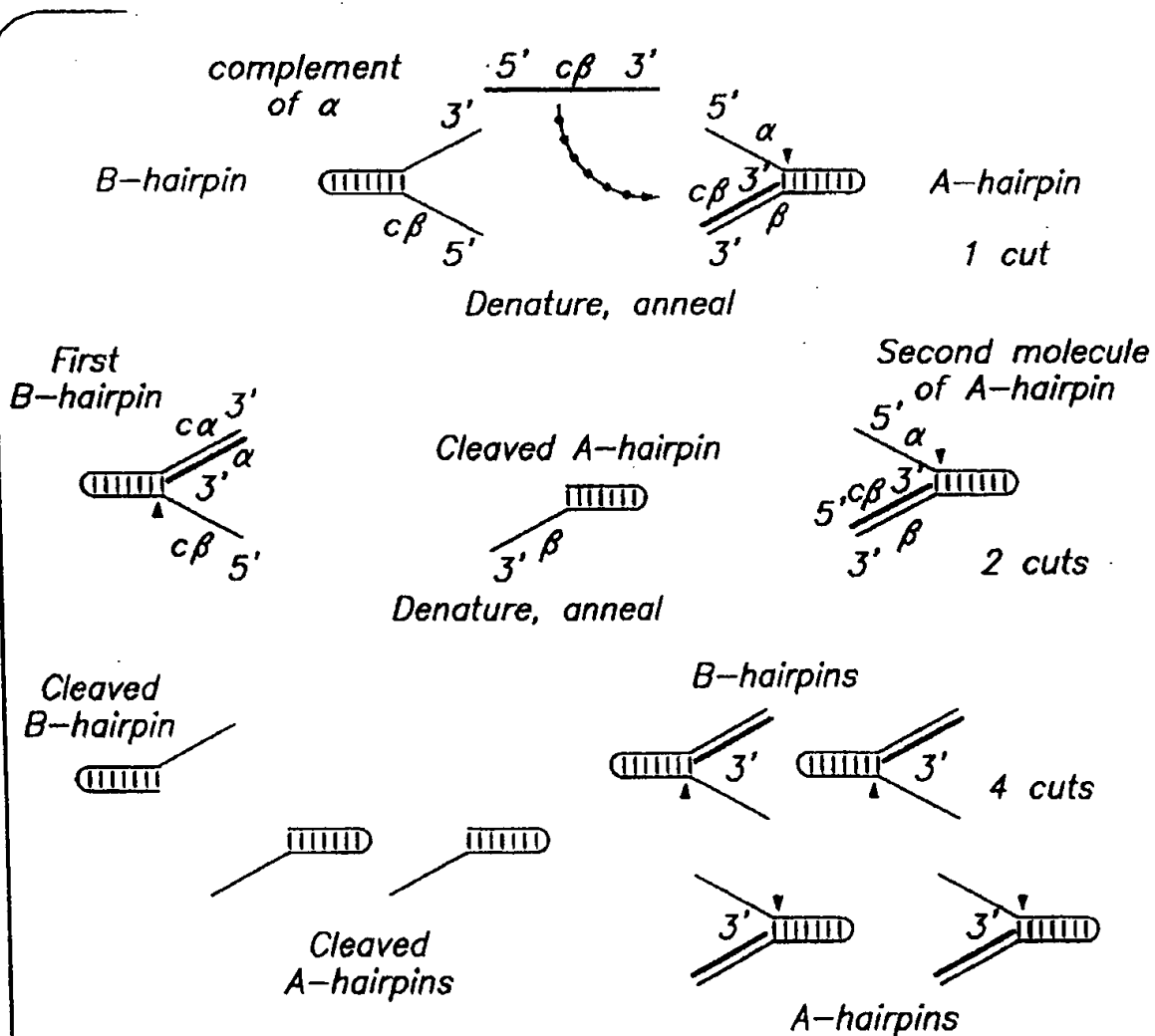


FIG. 1C PART TWO: DETECTION REACTION

FIG. 2A

MAJORITY [SEQ ID NO:7]	ATGXXGGGGATGCTTCCGCTCTTTGAGCCCAAGCCCGGGTCTCTGCTGGTGGACGGCCACCGACCTGGCCT	
DNAPTAA [SEQ ID NO:1]	...AG..G.....G.....G.....	70
DNAPTFL [SEQ ID NO:2]C..G.....	67
DNAPTTH [SEQ ID NO:3]	...GA.....G.....A.....	70
MAJORITY	ACCGGAGCTTCTTCCGCTGAGGGCTCAGCAGCCAGCCGGGGGAAACCGGTGCAGGGCGGTCTACGGCTT	
DNAPTAACA.....G.....G.....	140
DNAPTFLT.....C.....G.....G..T.....	137
DNAPTTHG.....G.....	140
MAJORITY	CGCCAAAGAGGCTCTCAAGGCCCTGAAGGAGGACGGGGACXXGGGGGTGTCGTGGTCTTTGAGCGCCCAAG	
DNAPTAAC.....A.....	207
DNAPTFLA.....GT..T.....	204
DNAPTTHT..AA..C..CT.....	210
MAJORITY	GGCGGCTCCTTCCGGCAGAGGCTACGAGGCTAGAAAGCGGGCCCGGGCCCGCCCGGAGGACTTTC	
DNAPTAAG..GG.....G.....	277
DNAPTFLGA.....C.....C.....C..	274
DNAPTTH	280
MAJORITY	CCCGGCGAGCTCGGCTCATCAAGGAGCTGGTGGACCTCCTGGGGCTTGGCGGGCTCGAGGTCCTCCCGGGCTA	
DNAPTAAA.....G.....G.....G.....	347
DNAPTFLG.....T.....A..G.....T..G..G.....T.....	344
DNAPTTHT..A.C.....	350

FIG. 2B

MAJORITY [SEQ ID NO:7]	CGAAGCGGACGAGGTCTGCGCCACCCCTGCGCAAGAAAGGCGGAAAGGAGGCTACGAGGTCCGCGCATCCTC	
DNAPTAQ [SEQ ID NO:1]C.....G.....C.....C.....	417
DNAPTFL [SEQ ID NO:2]	T.....G.....CG.....	414
DNAPTTH [SEQ ID NO:3]T..C.....	420
MAJORITY	ACCGCGGACCGGACGCTCTACGAGCTCCTTCCGAGCCGCACTCGCGCTCCTCCACCCGAGGCGTACCTCA	
DNAPTAQAAA.....T.....CA.....	487
DNAPTFL	..T.....G.....G.....A.....T.....G..	484
DNAPTTHA..G.C.....G.....CG.....	490
MAJORITY	TCACCCCGGCGTGGCTTGGGAGAACTAGGCGCTGAGGCGGAGCACTGGGTGGACTACCGGCGGCTGGC	
DNAPTAQC.....A.....C..C.....CG.....A..	557
DNAPTFLAC.....C.C.....	554
DNAPTTHA.....C.....T..C.....C.T..	560
MAJORITY	GGGCGACCGCTCGGACACCTCCCGGGGTCAAGGGCATCGGGGAGAGACCGCCCGAAGCTCCTCXAG	
DNAPTAQ	C.....GAG.....T.....G..GAG.....T..GG..	627
DNAPTFLG..T..A.....G.....A..G.....A..CGC	624
DNAPTTHTC.....A..	630
MAJORITY	GAGTGGGGAGCCCTGGAAACCTCCTCAAGAACCTGGACCGGCTGAAGCCCGC...CXTCGGGAGAGACA	
DNAPTAQGC.....C.....A.....	694
DNAPTFLT..C..C.....A.....T..T..G.....C	691
DNAPTTHA.....A.....A..AAAA.G.....	700

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FIG. 2C

MAJORITY [SEQ ID NO:7]	TCCAGGCCCCACATGAXGACCTGAXGCTCTCCTGGGAGCTXTCCGAGGTCCGACCGACCTGCCCTGGA	
DNAPTAQ [SEQ ID NO:1]C..T....A.....C..GG..A.....	764
DNAPTFL [SEQ ID NO:2]GGG.....G.C....GCC..T...C..A....T.....A..T.....	761
DNAPTH [SEQ ID NO:3]A.....C.....A.....C.G.....T.....C....G.....C.....	770
MAJORITY	GGTGGACTTCGCCAAGXGGGGGAGCCCGACCGGAGGAGGCTTCTGGAGAGGCTGAGCTT	
DNAPTAQAA.....A.....A.....A.....T.....	834
DNAPTFLGG.G.C.C.CACA...A..T.....T...GC...T...C..T.....	831
DNAPTHC.....C.G.....G.....G.....C.....C.....	840
MAJORITY	GGGAGCCTGCTCCAGGAGTTCGGGCTCCTGGAGGGCCGCAAGCCCTGGAGGAGGCCCCCTGCCCGCCGC	
DNAPTAQT.....AA.....	904
DNAPTFLA.....G..G...GGCA.....	901
DNAPTHG.....C...GGCC.....	910
MAJORITY	CGGAGGGGCTTCGTGGGCTTTGTCTTCGGGGCGGAGGCCCATGTGGGGCGAGCTTCTGGCCCTGGC	
DNAPTAQG.....AAG.....T.....	974
DNAPTFLT..T.....TC.T.....T.....	971
DNAPTHG.....C.....G.....AAA.....	980
MAJORITY	CGCGGGCAGGGAGGGGGGCTCGACGGGGGACGACCGCTTAXGGGGCTXAGGGGACCTXAGGGAGGTG	
DNAPTAQG.....C..C..G..T.A..AA.G..G.....G.....C.....	1044
DNAPTFL	T.GG..GT.....G..CC...T.....A.....C..G...G.....T.....G.....	1041
DNAPTHTG.....C.....G.....G.....GCG...G..A.A.....C.....C.....	1050

.....	G. C.	T. AG.	T. G.	C. 1394
GG.....	C.		C.	A. C 1391
.....	C. A.	T.	T.	C. T. 1400

FIG. 2E

MAJORITY [SEQ ID NO:7]	GGAGATCCGCCCTCGAGGAGGCTTCCGCCCTGGCCGCGCCGCTTCAACCTCAAGTCCCGGGAG	1454
DNAPTAA [SEQ ID NO:1]GC.....CC.....	1461
DNAPTFL [SEQ ID NO:2]G.G.....AG.G.....	1470
DNAPTTH [SEQ ID NO:3]T.....G.....	
MAJORITY	CAGCTGGAAAGGCTGCTCTTTGACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGGACXGGCAAGC	
DNAPTAAC.....A.....	1534
DNAPTFLGC.....G.C.G.T.....	1531
DNAPTTHTA.....T.G.G.....C.A.....	1540
MAJORITY	GCTCCAGGAGGCGCGCTGCTGGAGGCGCTXCGXGAGGCGCCACCCCATCGTGGAGAGATCCTGCAGTA	
DNAPTAAG.....C.....C.....	1604
DNAPTFLT.....G.A.....CCG.....	1601
DNAPTTHG.....A.G.....C.....C.....	1610
MAJORITY	CGGGGAGCTCAGCAAGCTCAAGAACACCTACATXGAGCCGCTGCGXGCTGCTCGACCGCAGGAGCGGGC	
DNAPTAAG.....T.....T.....G.A.....A.....	1674
DNAPTFLA.....C.C.....G.....A.....C.....	1671
DNAPTTHG.G.....C.AAG.....G.....	1680
MAJORITY	CGCCTCCAGACCGGCTTCAAGCAGACGCGCCACGCGCCACGCGCTTAGTAGCTCGGACCGCCAGCCTGC	
DNAPTAAA.....T.....C.....	1744
DNAPTFLG.....C.....TCC.....	1741
DNAPTTHG.....	1750

FIG. 2F

MAJORITY [SEQ ID NO:7]	AGAACATCCCCGCTCCGCACCCXCTGGGCGAGAGGATCGGCGGGGCTTCGTGGCCGAGAGGAGGXTGGGT	
DNAPTAQ [SEQ ID NO:1]G..T..G.....A..C.....G...C..	1814
DNAPTFL [SEQ ID NO:2]G.....T.....C..C.....A.....C.....	1817
DNAPTTH [SEQ ID NO:3]CT.....C.....C.....T.....C.....	1820
MAJORITY	GTGGTGGCCCTGGACTATAGCCAGATAGAGGTCGGGGTCGTGGCCGACGGTCTCCGGGGACGAGAACCTG	
DNAPTAQ	A.....A.....A.....G.....C.....	1884
DNAPTFL	C.....T..T.....G.....T.....T.....C.....	1881
DNAPTTHC.....C.....C.....C.....A.....	1890
MAJORITY	ATCGGGGTCTTCAGGAGGGAGGACATCCACACCCAGAGCGGGCAGCTGGATGTTGGGGTCCCCCGGG	
DNAPTAQG.....G.....G.....G.....G...	1954
DNAPTFLT.....T.....T.....T.....T.....C...	1951
DNAPTTH	A.....A.....A.....A.....A.....	1960
MAJORITY	AGGGCGTGGACCCCTGATCGCCGGGGGGCCAGACCATCAAGTTCGGGGTCCCTCTAGGGCATGTCCGG	
DNAPTAQG.....G.....G.....G.....G...	2024
DNAPTFL	A..G..A.....T.....G.....G.....	2021
DNAPTTHGG..G.....C.....C.....	2030
MAJORITY	CCACGGCCCTCTCCGAGGAGCTTGGCATCCGCTACGAGGAGGGGGTGGCCCTTCATTGAGGGCTACTTCCAG	
DNAPTAQA.....T.....CCA.....T...	2094
DNAPTFLGG.....T.....T.....T.....	2091
DNAPTTH	...TA..G.....T.....T.....A.....A	2100

FIG. 2G

MAJORITY [SEQ ID NO:7]	AGCTTCGGCAAGGTGCGGCGCTGGATTGAGAGACCTGGAGGAGGCGGCGGCTACGTGGAGA	2164
DNAPTAQ [SEQ ID NO:1]	2161
DNAPTFL [SEQ ID NO:2]	A.....GG.....C.....CG.....T.....	2170
DNAPTTH [SEQ ID NO:3]A.....A.....G.....A.....C.....A.....	
MAJORITY	CCCTCTTCGGCGCGCGGCGCTACGTGCGCGAGCTCAAGCGCGCGGTTGAAGAGCGTCCGGGAGCGCGCGGGA	
DNAPTAQC.....A.....AG.G.....C.....	2234
DNAPTFLT.....C.....	2231
DNAPTTH	AA.AA.....CA.....C.....	2240
MAJORITY	CGCGATGGCGCTTCAAGATGGCGGTCCAGGGCGACCGCGCGCGACCTCATGAAGCTGGCGATGGTGAAGCTC	
DNAPTAQT.....T.....	2304
DNAPTFLG.....CG.....T.....	2301
DNAPTTHC.....	2310
MAJORITY	TTCCCGCGGCTXCAAGGAAATGGGGGCGCAGGATGCTGGTCAAGGTCCAGGACGAGCTGGTCTCGAGGCGCG	
DNAPTAQA.....GG.....T.....	2374
DNAPTFLT.....C.....G.....TT.G.....G.....	2371
DNAPTTHC..C.G..G.....C.G.....C.....CC.....G.....	2380
MAJORITY	CCAAAGAGCGCGCGGAGGCGXGGTGGCGGCTTTGGCCAAAGAGGTCATGGAGGGGCTCTATCCCGTGGCGGT	
DNAPTAQ	A.....A.....CC.....CGGC.....G.....	2444
DNAPTFLG..C.....AG...A.....GG.....CAG...	2441
DNAPTTHC...C.....C...A.....G.....AA..C.....C.....	2450

FIG. 2H

MAJORITY [SEQ ID NO:7]	GGCCCTGGAGGTGGACGTGGGGATGGGGGAAGACTGGCTCTCGGGCCAAAGGAGTAG	
DNAPTAG [SEQ ID NO:1]A.....	GA 2499
DNAPTFL [SEQ ID NO:2]CC.....	2496
DNAPTTH [SEQ ID NO:3]T.....GT...	2505

FIG. 3A

MAJORITY [SEQ ID NO: 8]	MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGPVQAVYGFAKSLIKALKEDG·DAVXVVVFDK	
TAQ PRO [SEQ ID NO: 4]	RG.....H.....	69
TFL PRO [SEQ ID NO: 5]V.....V.....V.....	68
TTM PRO [SEQ ID NO: 6]	E.....YK.....F.....	70
MAJORITY APSFRHEAYEAYKAGRPTPEDFPROLALIKELVDLGLXRLEVPOYEADOVLATLAKKAEKEGYEVRIL		
TAQ PRO	GG.....A.....S.....	139
TFL PROV.....F.....R.....	138
TTM PROFT.....	140
MAJORITY TADRDLYOLLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPSONLPGVKGI GEKTAXKLLX		
TAQ PRO	K.....H.....D.....T.....E.....R.....E	209
TFL PROE.....I.....Y.....A.....I.....QR.....IR	208
TTM PRO	V.....V.....H.....E.....F.....V.....L.....K	210
MAJORITY EWGSLNLLKNLDRVNP·XXREKIXAHMEDLXLSXXLSXVRTOLPLEVDFAXRREPDRGLRAFLERLEF		
TAQ PRO	A.....L.....AI.....L.....D.....K.....WD.....AK.....K.....R.....	278
TFL PROFQH.....Q.....SL.....LQ.....G.....A.....RK.....G.....H.....GR.....T.....NL.....	277
TTM PROENV.....K.....L.....R.....LE.....R.....L.....OG.....	280
MAJORITY GSLLHEFGLLXPKALEEAPWPPPEGAFVGFVLSRPEPMHAEALLAARXGRVHRAXDPLXGLRDLKEV		
TAQ PRO	S.....S.....K.....D.....G.....PE.....YKA.....A	348
TFL PROG.....A.....L.....SF.....L.....G.....WE.....L.....Q.....R.....G	347
TTM PROA.....AP.....K.....C.....D.....A.....A.....K.....	350

FIG. 3B

MAJORITY	[SEQ ID NO: 8]	RGLIAKDLAVLALREGLDIXPGDDPMLLAYLLDPSNTTPEGVARRYGGWTEGAGERALLSERLFXNLXX	
TAQ PRO	[SEQ ID NO: 4]	S.....G.P.....A.....A.....WG	418
TFL PRO	[SEQ ID NO: 5]	I.....F.E.....A.....OT.KE	417
TTM PRO	[SEQ ID NO: 6]	S.....V.....AH.....HR..LK	420
MAJORITY		RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRLEEEVFRLAGHPFNLNSRD	
TAQ PRO		R...R...A.....R.....A.....A.....	488
TFL PRO		K.....E.....R.....EA.V.Q.....	487
TTM PRO		K.....H.....L.....L.....	490
MAJORITY		QLERVLFDELGLPAIGTEKTGRSTSAAVLEALREAHPIVEKILQYRELTCLKNTYIDPLPXIVHPRTG	
TAQ PRO	S.....D.I.....	558
TFL PRO	DR.....A.....K.....	557
TTM PRO		R...L...Q.....H.....V.....S.....	560
MAJORITY		RLHTRFNOTATATGRSSDPNLDNI PVRTPLGQRI RRAFVAEEGWXLVALDYSOIELRVLAHLSGDENL	
TAQ PRO	I.....L.....	628
TFL PRO	V...V.....	627
TTM PRO	A...A.....	630
MAJORITY		IRVFQEGARDIHTQTASWMFGVPPEAVOPLMRAAKTINFGVLGYGMSAHLRSOELAI PYEEAVAFIERYFQ	
TAQ PRO	E.....R.....D.....	698
TFL PRO	S...G.....G...S.....	697
TTM PRO	K.....V.....	700

FIG. 3C

MAJORITY [SEQ ID NO: 8] SFPKVRAWIEXTLEGGRRGGVETLFORRRYVPDLNARVKSUREAAERMAFNMPYOGTAADLMLKLAHVXL

TAQ PRO	[SEQ ID NO: 4]E.....	768
TFL PRO	[SEQ ID NO: 5]	Y.....G.....R.	767
TTH PRO	[SEQ ID NO: 6]K.....	770

MAJORITY FPRLEXMGARMQLQVHDELVLLEAPKXRAEXUAALAKEVMEGVYPIAVPLEVEVGXGEDWLSAKEX

TAQ PROE.....E...A...R.....I.....	833
TFL PROQ...L.....D...R.....W...Q...L.....	831
TTH PROR.....L....QA...E.....A...KA.....M.....G	835

Genes for Wild-Type and Pol(-)DNAPTaq

Domain
Coding Regions: 5' Nuclease

Polymerase

FIG. 4A

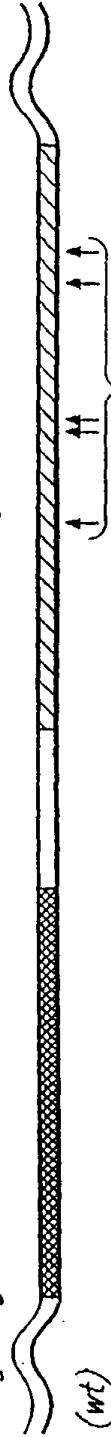


FIG. 4B



FIG. 4C



FIG. 4D



FIG. 4E

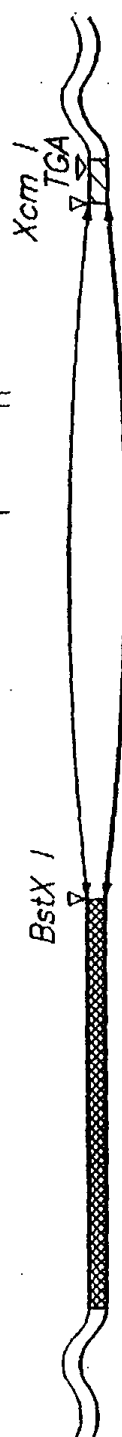


FIG. 4F

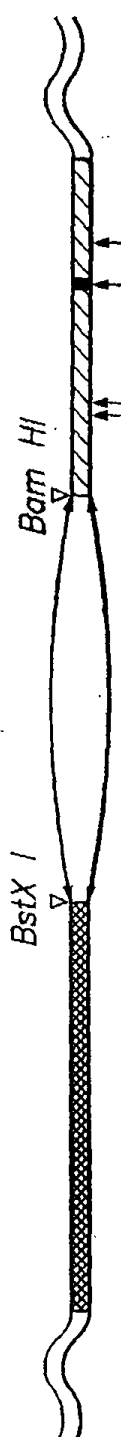
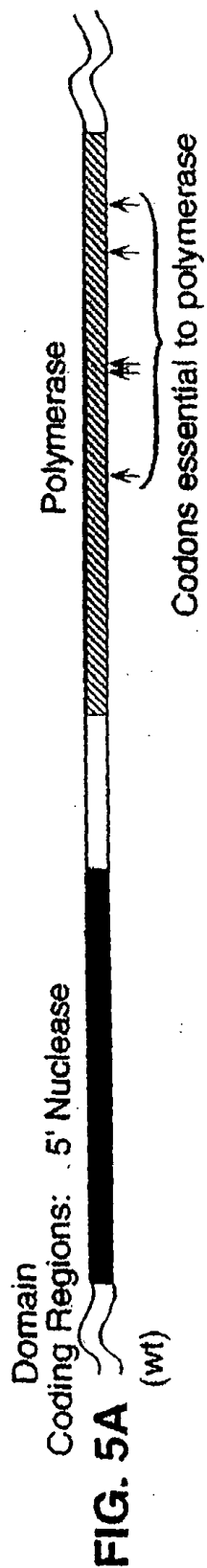


FIG. 4G



Genes for Wild-Type and Pol(-) DNAPTfl



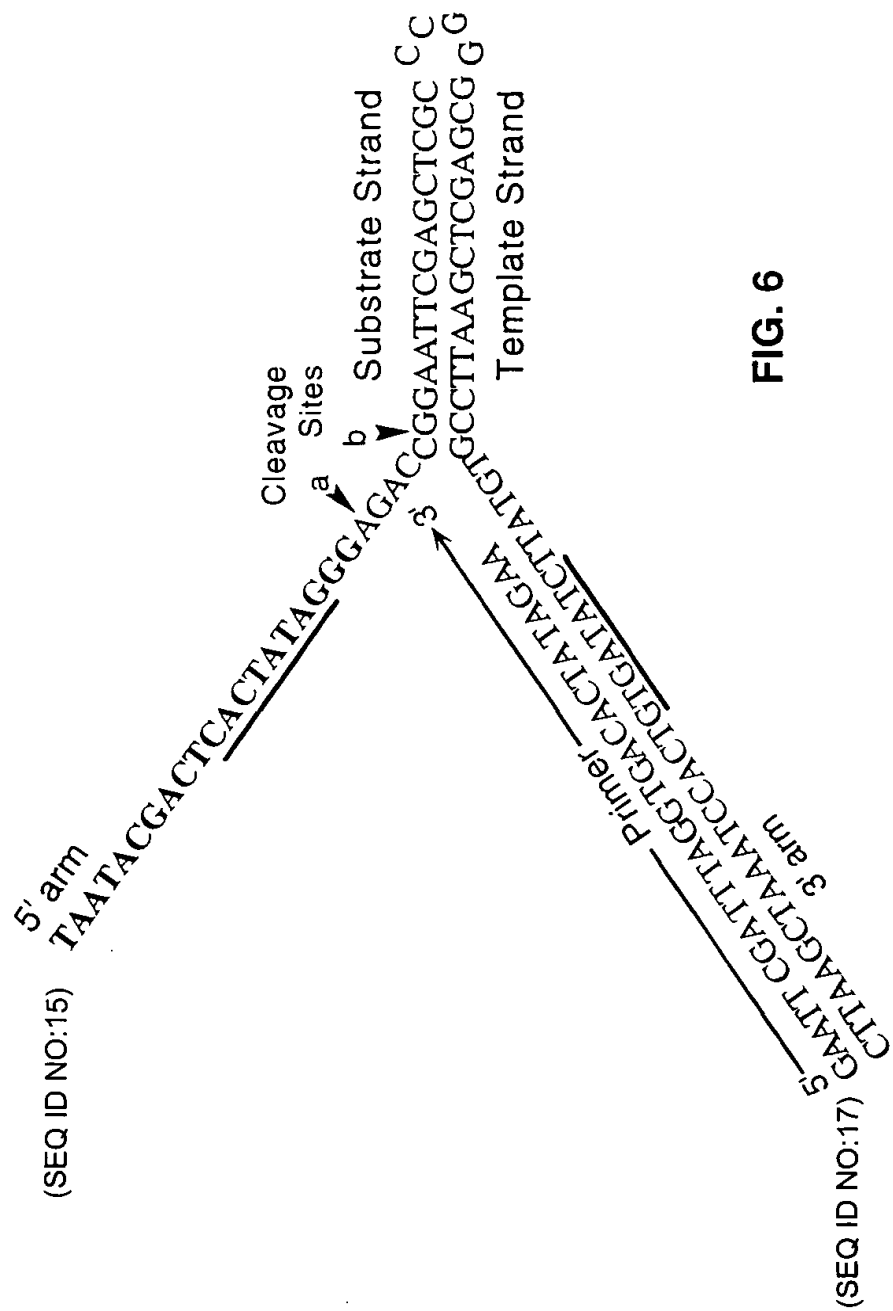


FIG. 6

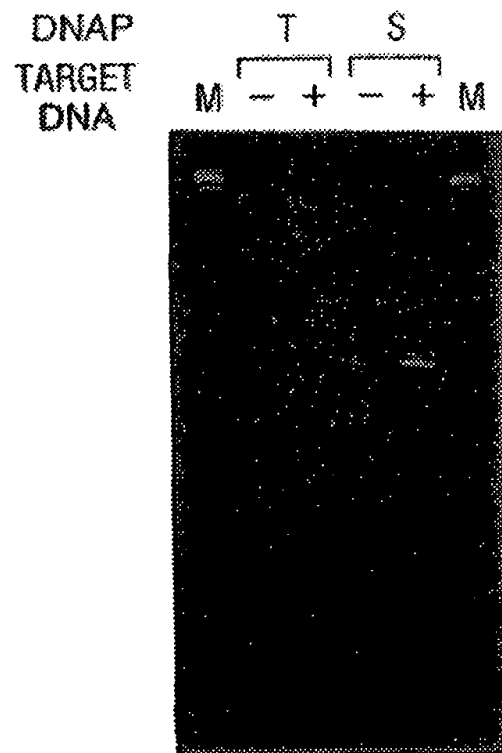


FIG. 7

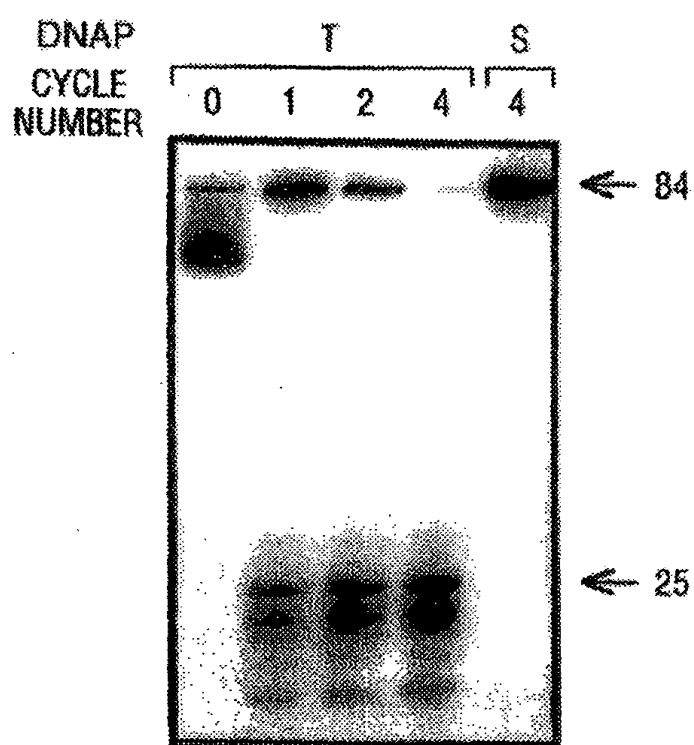


FIG. 8

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl ₂ :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

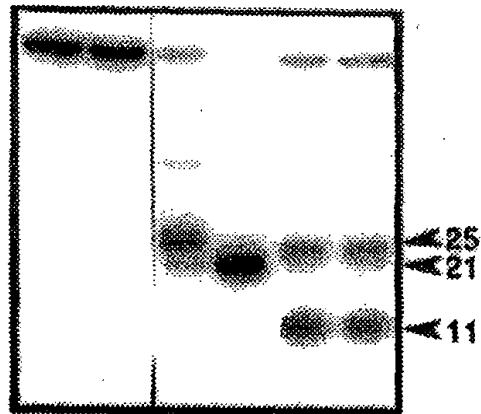


FIG. 9A

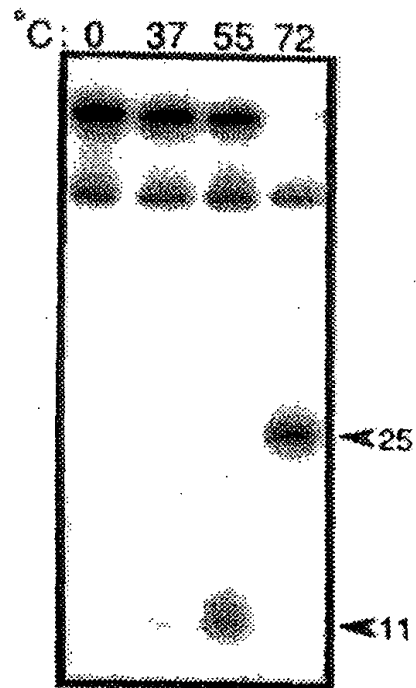


FIG. 9B

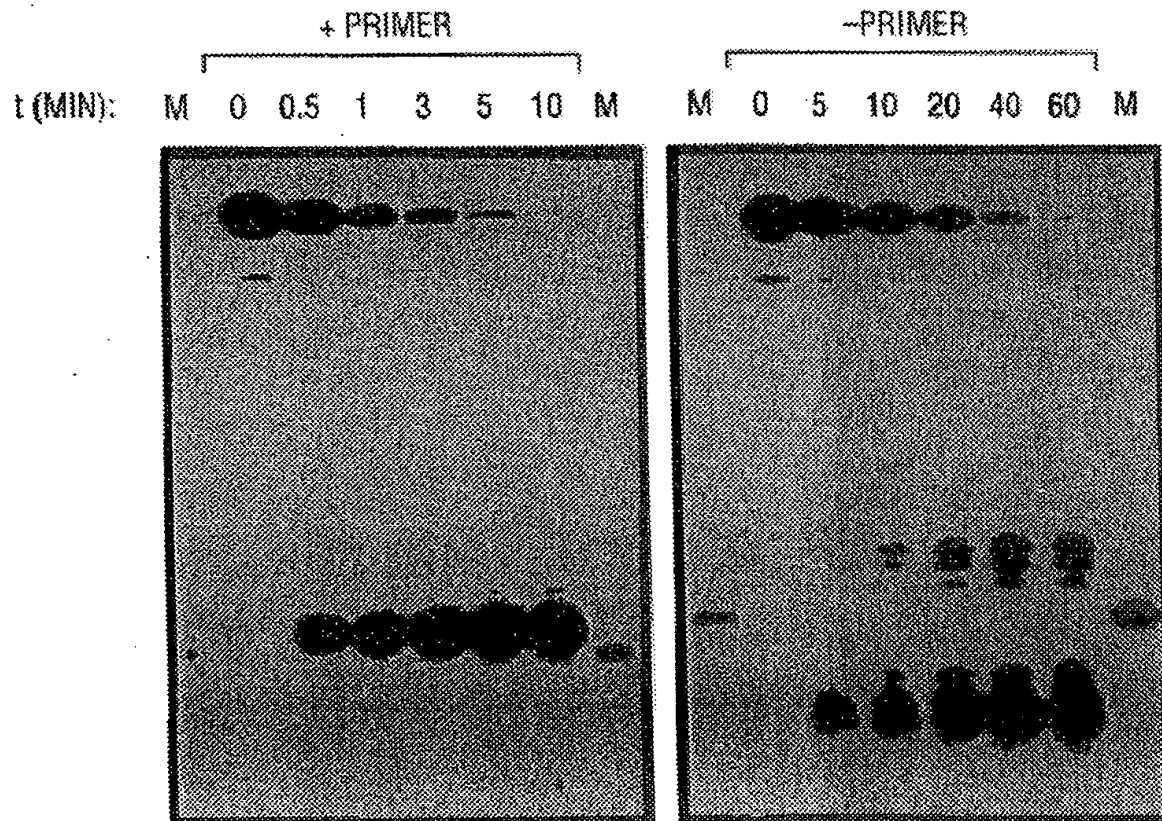
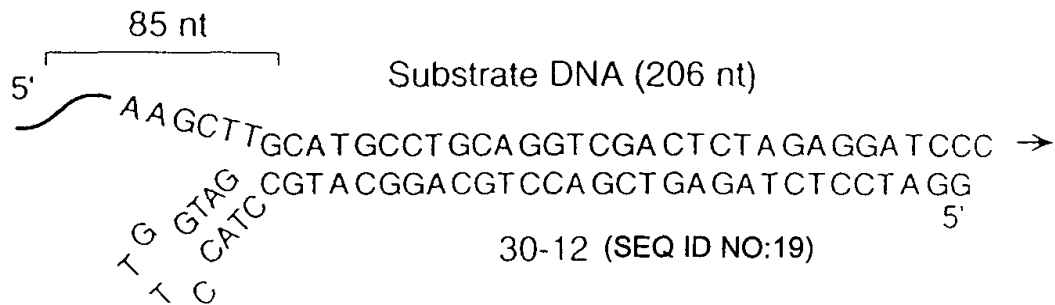
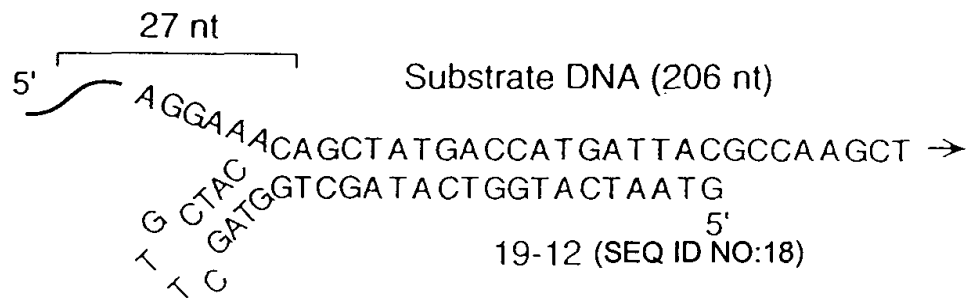


FIG. 10A

FIG. 10B



FIG. 12A



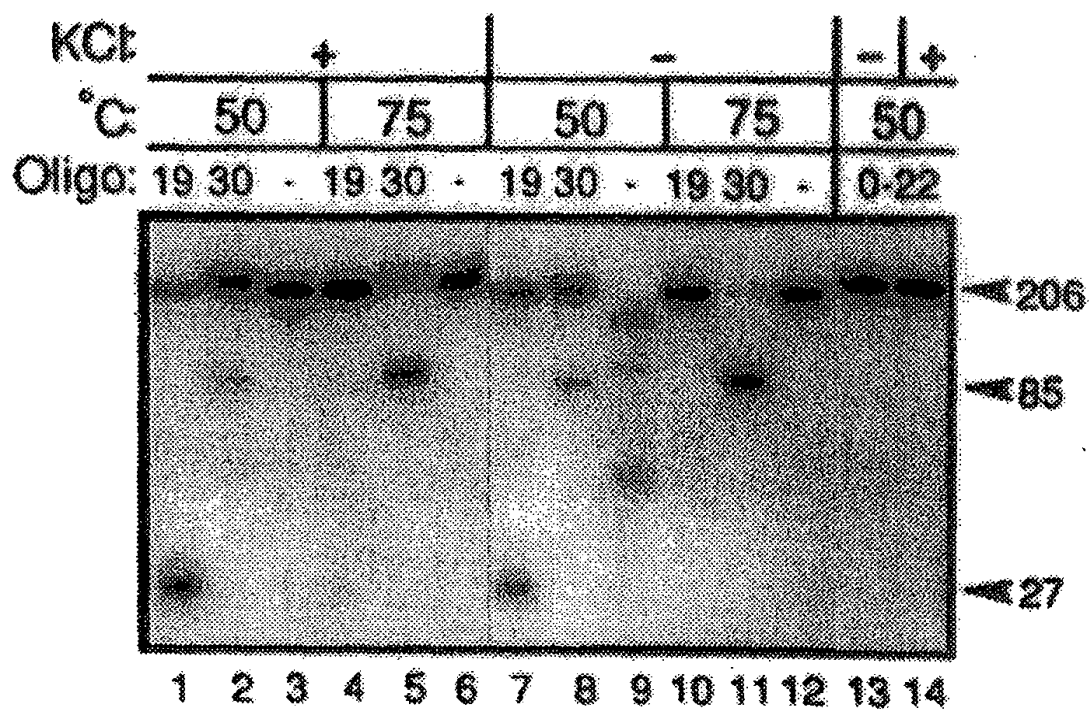


FIG. 12B

DNAP: - + +
30-0 : - - +

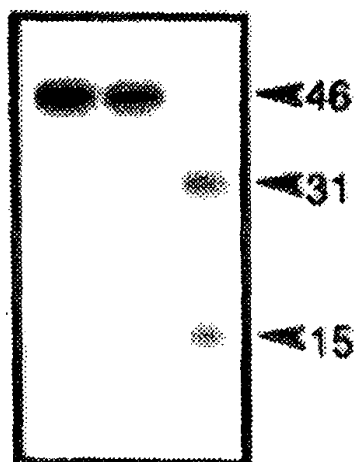
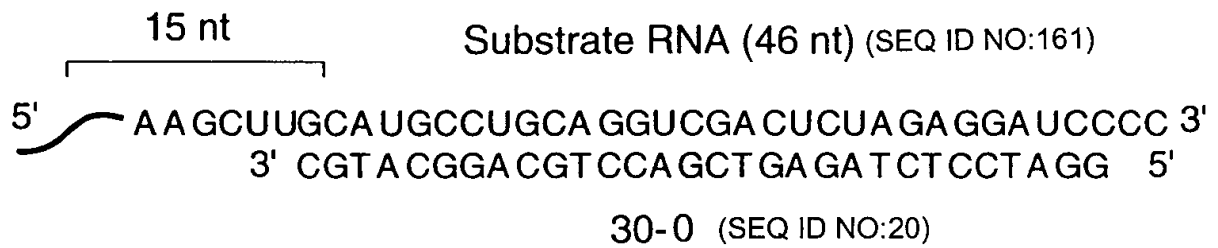


FIG. 13B

**FIG. 13A**

(SEQ ID NO:162)

-35
 TTGACAATTAAATCATCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCG
 -10
 MetAsnSer...
 ATGAATTCGAGCTCGGTACCCGGGGATCCTCTAGATCGACCTGCAGGCATGCAAGCTTGGCACTGGCC
 EcoRI _____ KpnI _____ BamHI _____ SalI _____ SphI _____ HindIII _____
 SstI _____ XbaI _____ PstI _____
 RBS

FIG. 14B

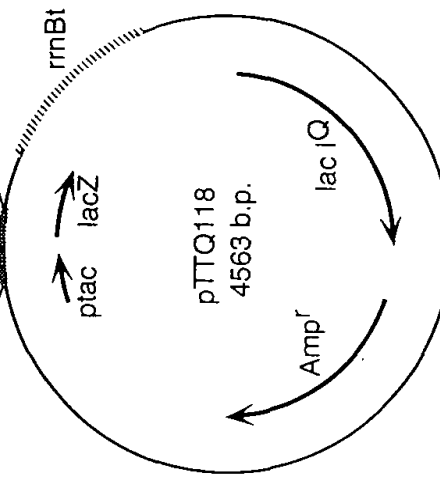


FIG. 14A

RBS: Ribosome binding site
ptac: Synthetic tac promoter
lac I^Q: Lac repressor gene
lacZ: Beta-galactosidase alpha fragment
rrnBt: E. coli rrnB transcription terminator

FIG. 14C

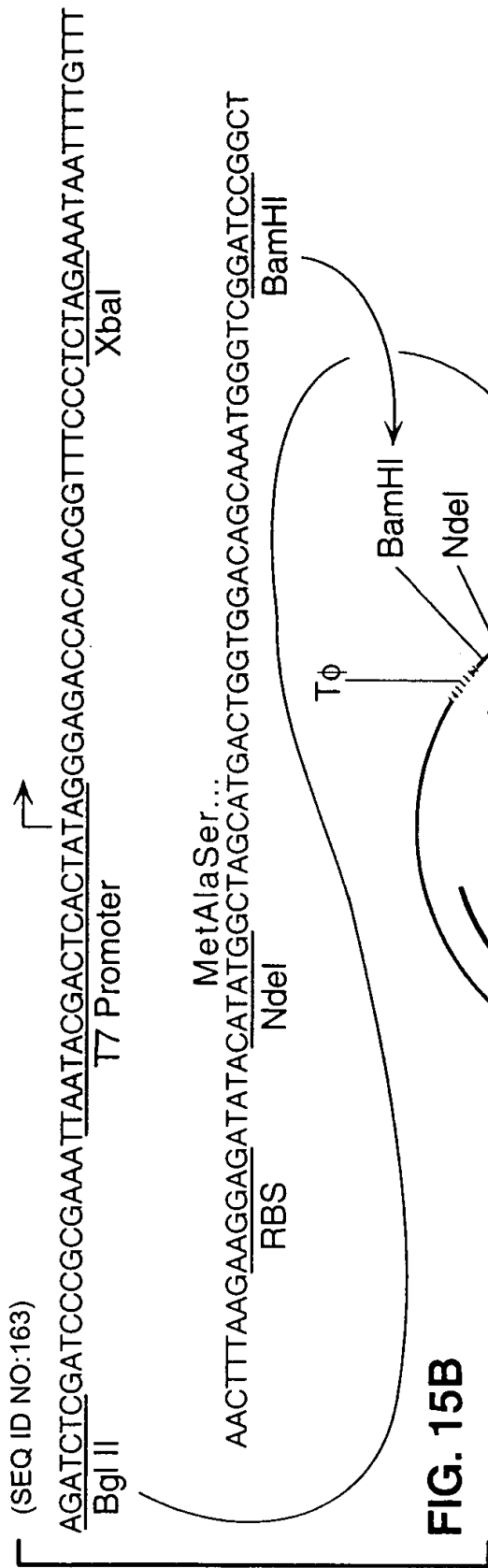


FIG. 15B

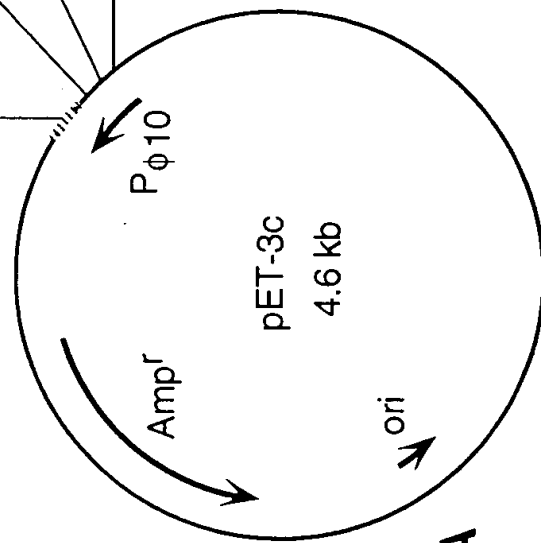


FIG. 15A

P_{φ10}: Bacteriophage T7 φ10 promoter RBS: Ribosome binding site
 Tφ: T7 φ Terminator

FIG. 15C

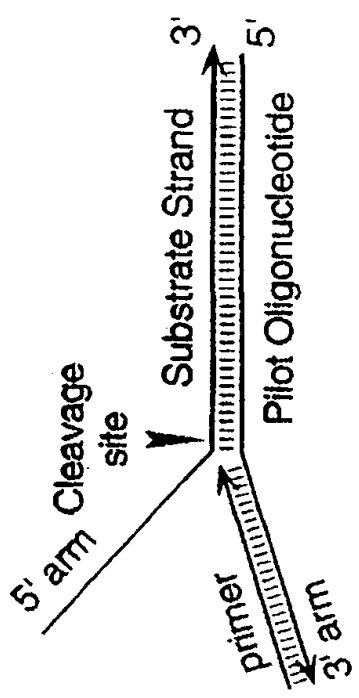


FIG. 16B

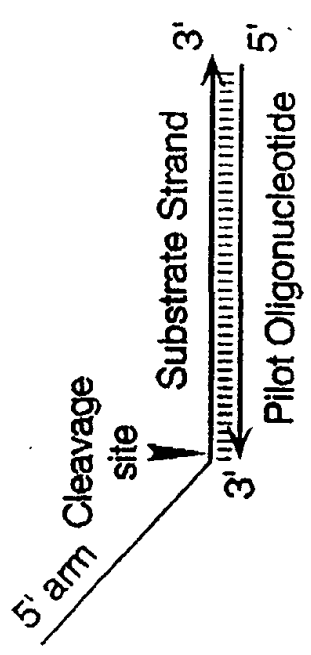


FIG. 16D

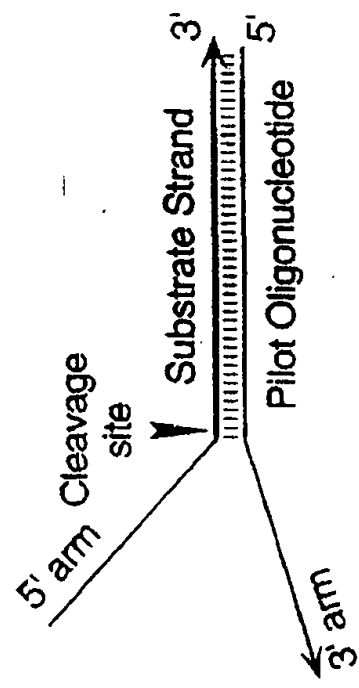


FIG. 16A

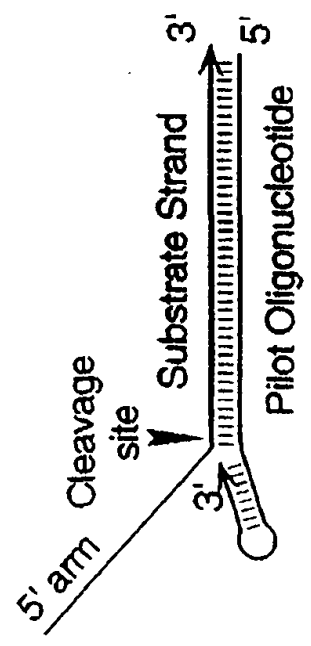


FIG. 16C

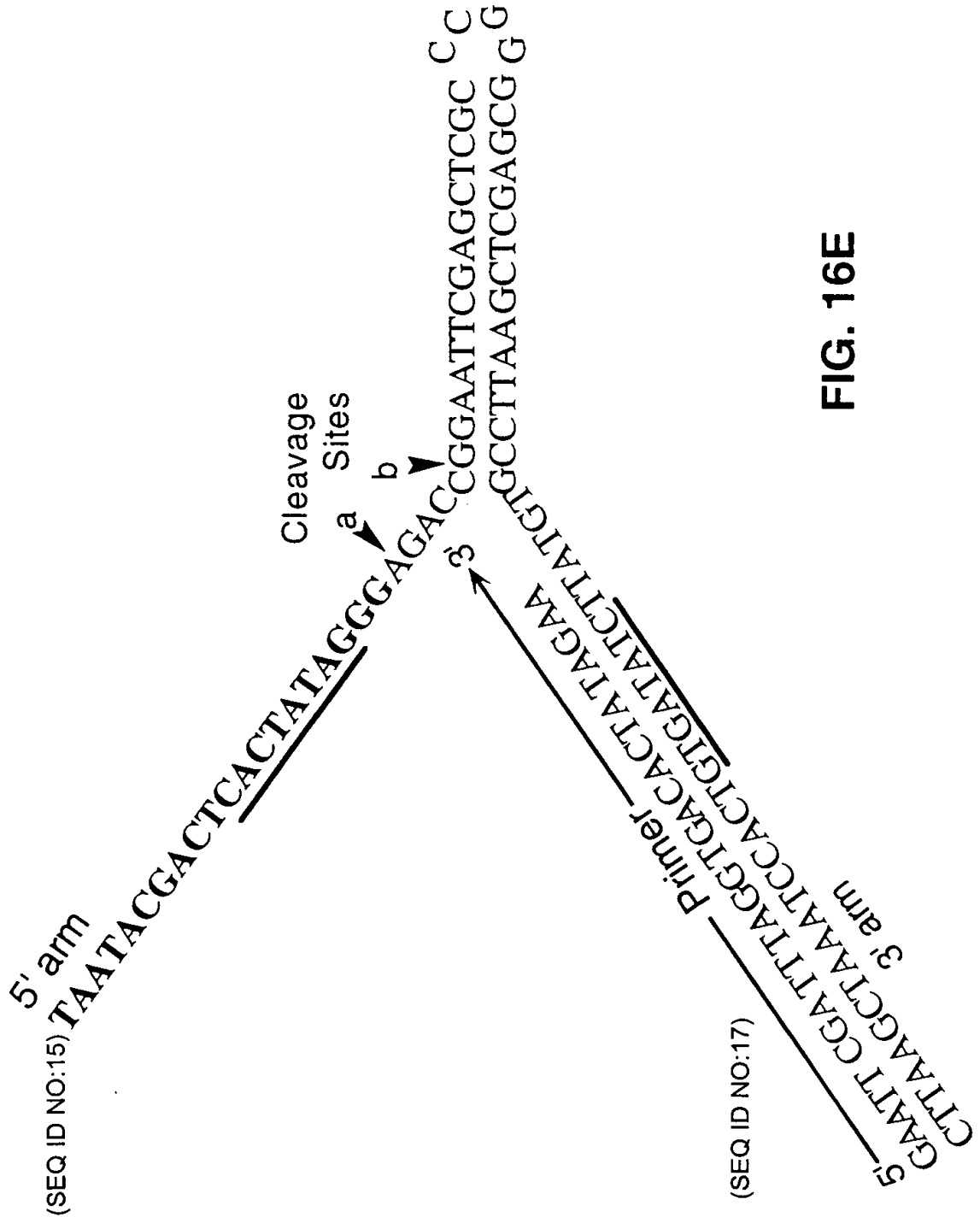
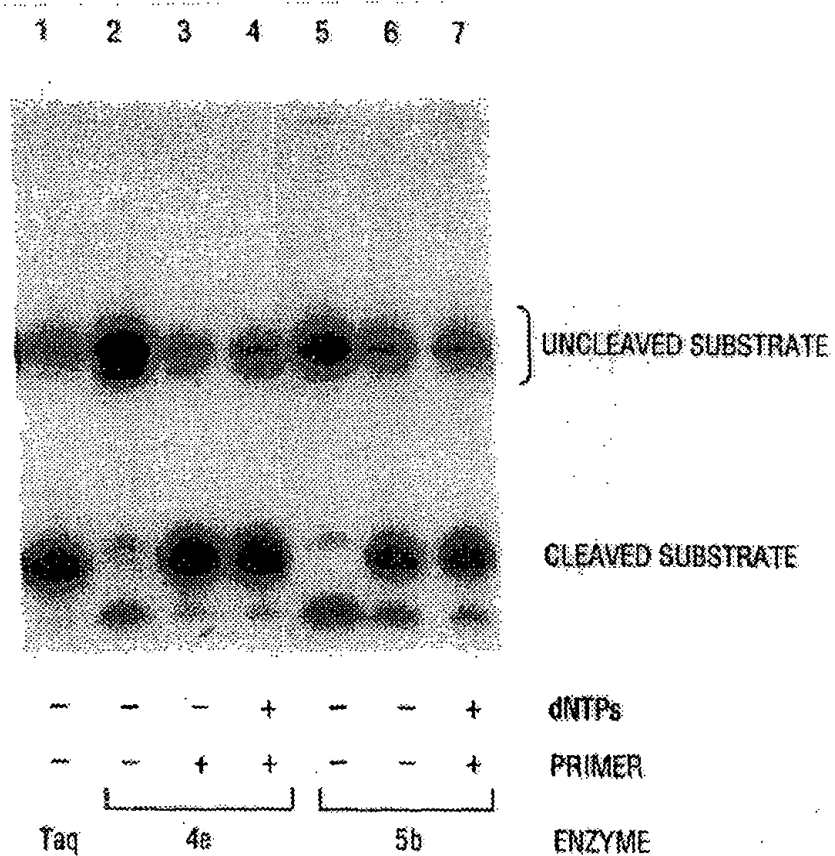


FIG. 16E

FIG. 17



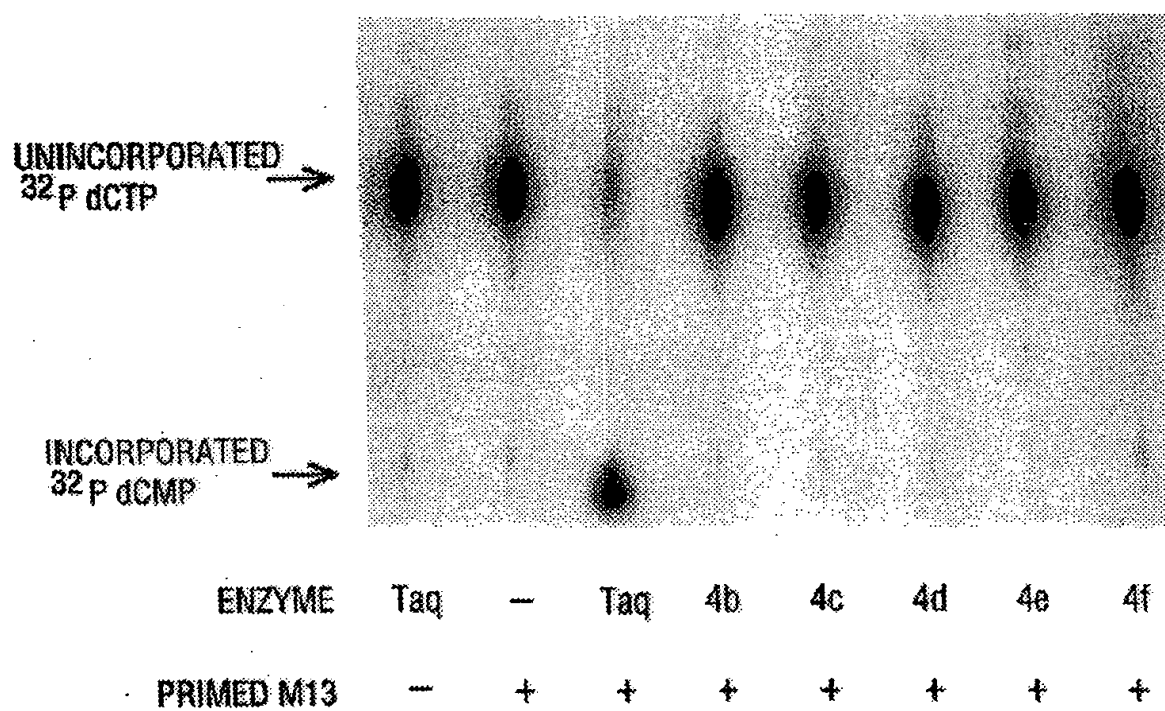


FIG. 18

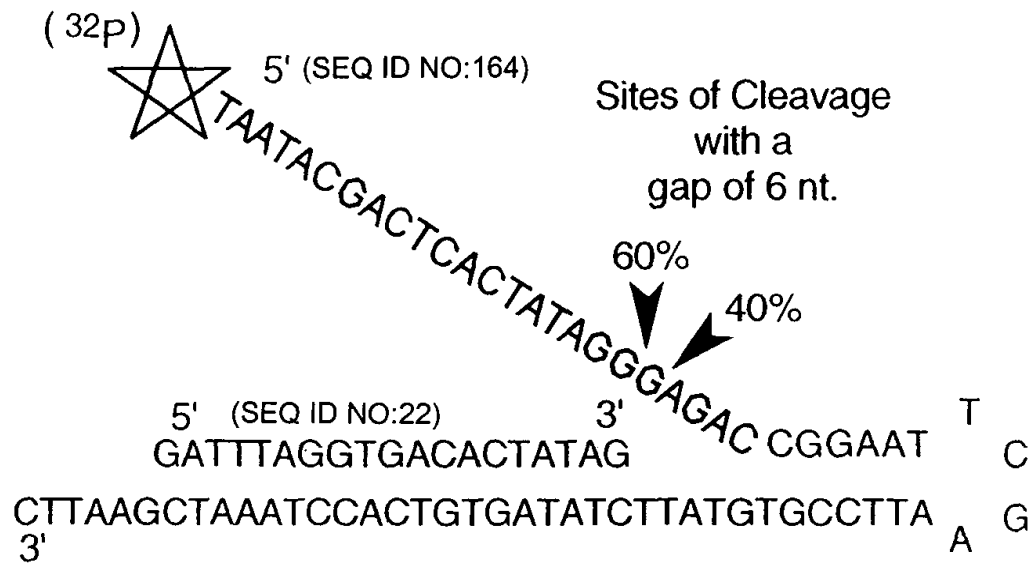


FIG. 19A

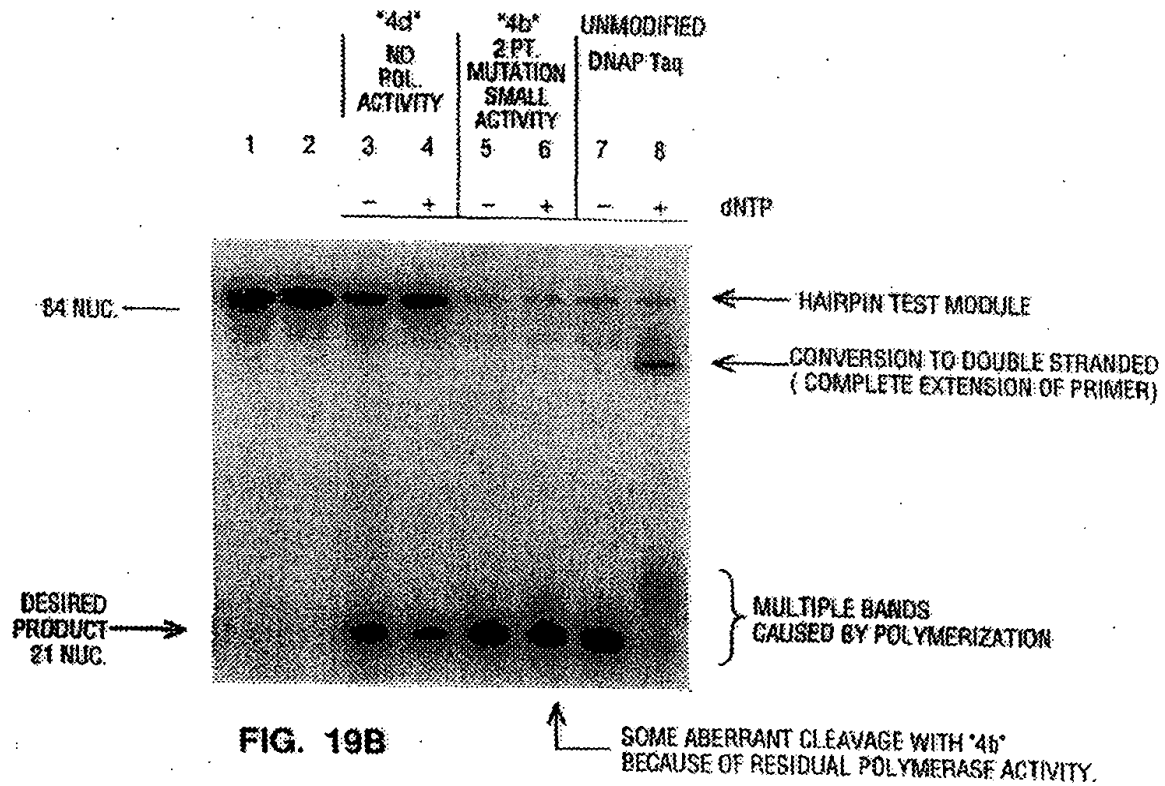


FIG. 19B

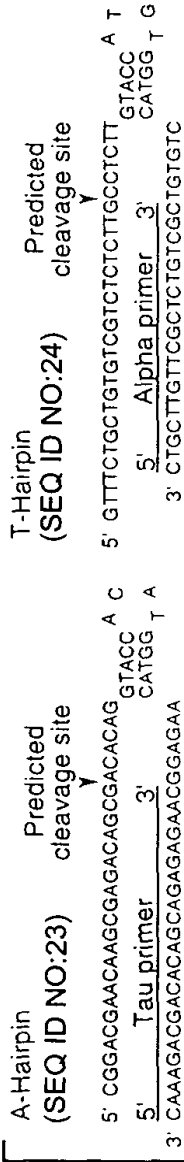


FIG. 20A

Sequence of alpha primer: (SEQ ID NO:25)
 5' GACGAAACGCGAGACAGCG 3'

FIG. 20B

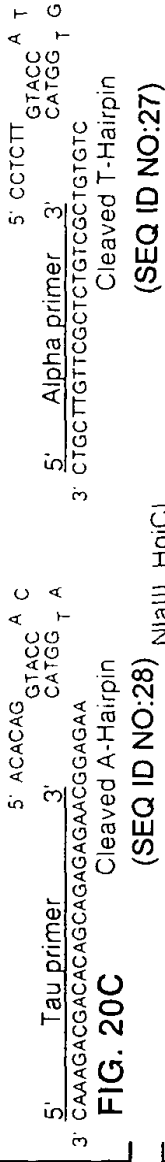


FIG. 20C

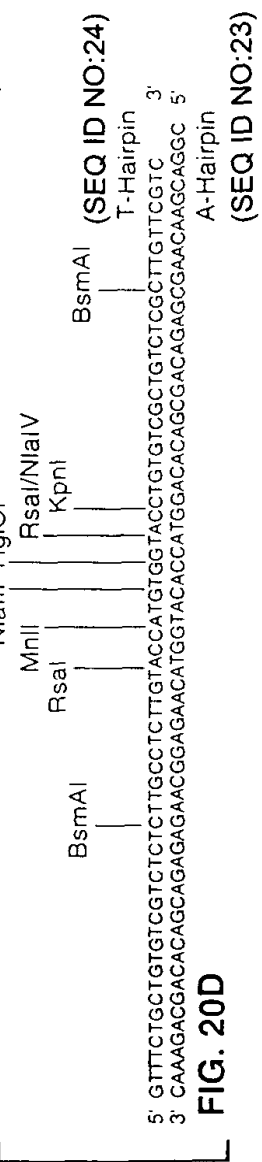


FIG. 20D

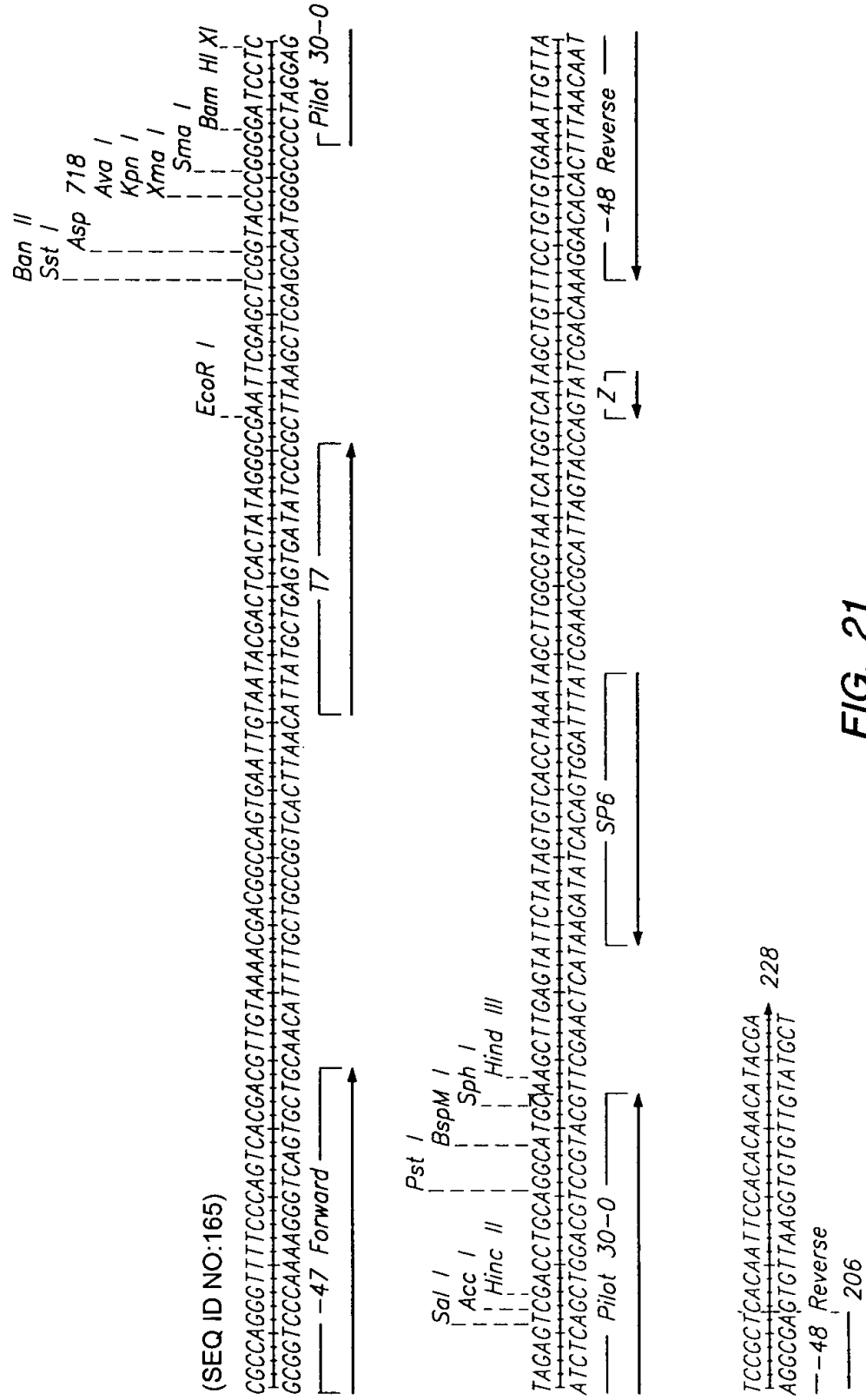
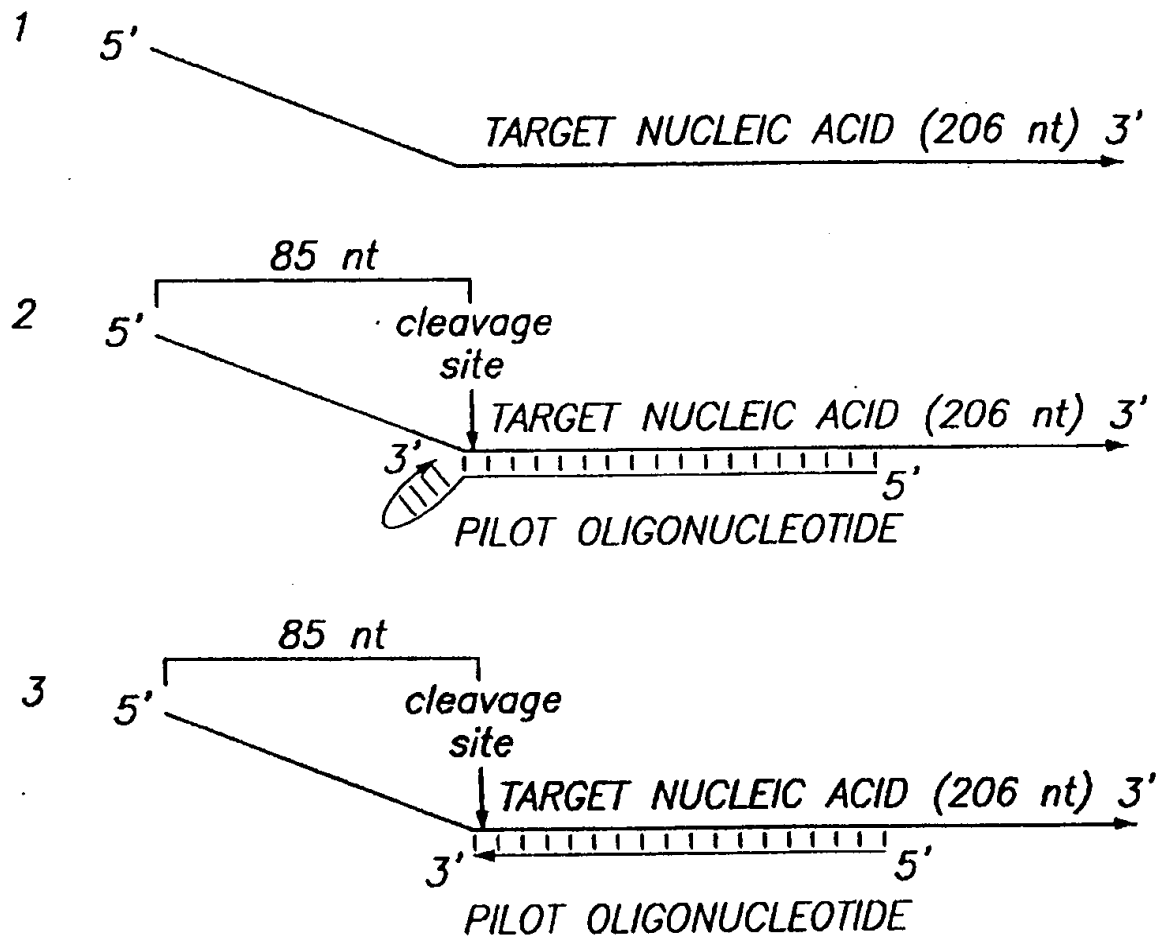


FIG. 21

**FIG. 22A**

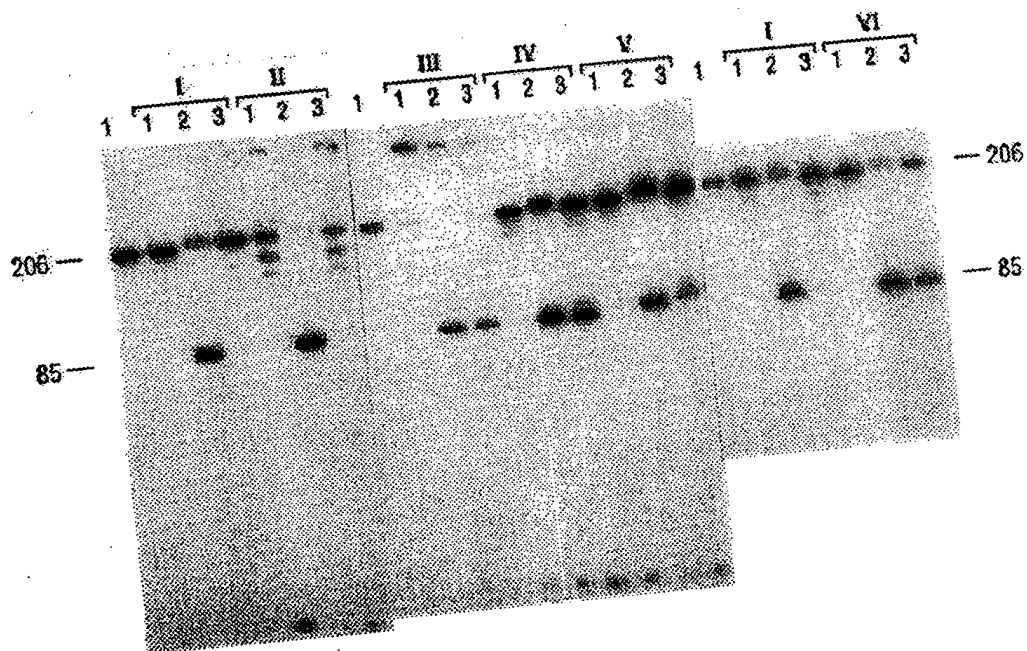


FIG. 22B

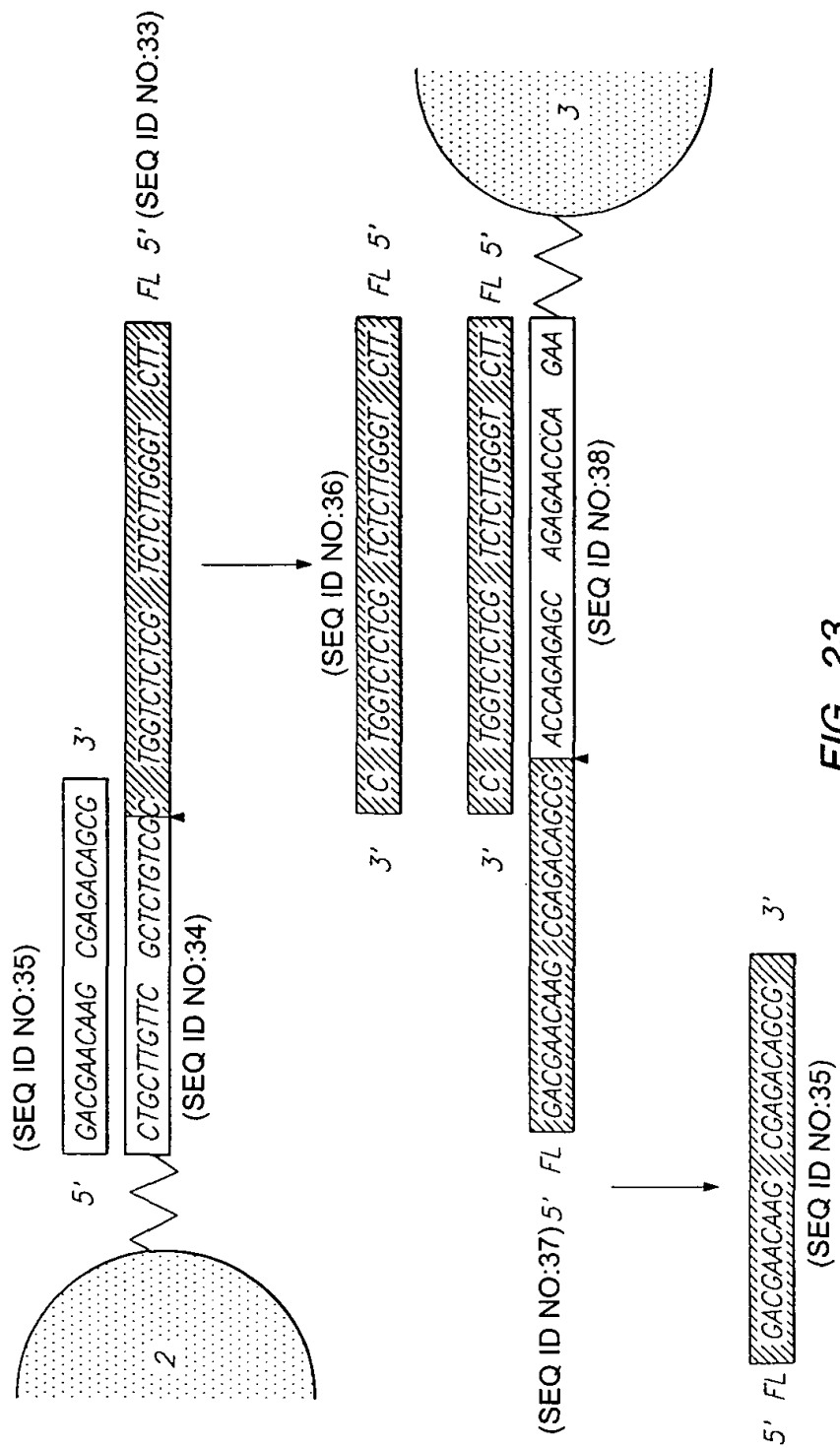


FIG. 23

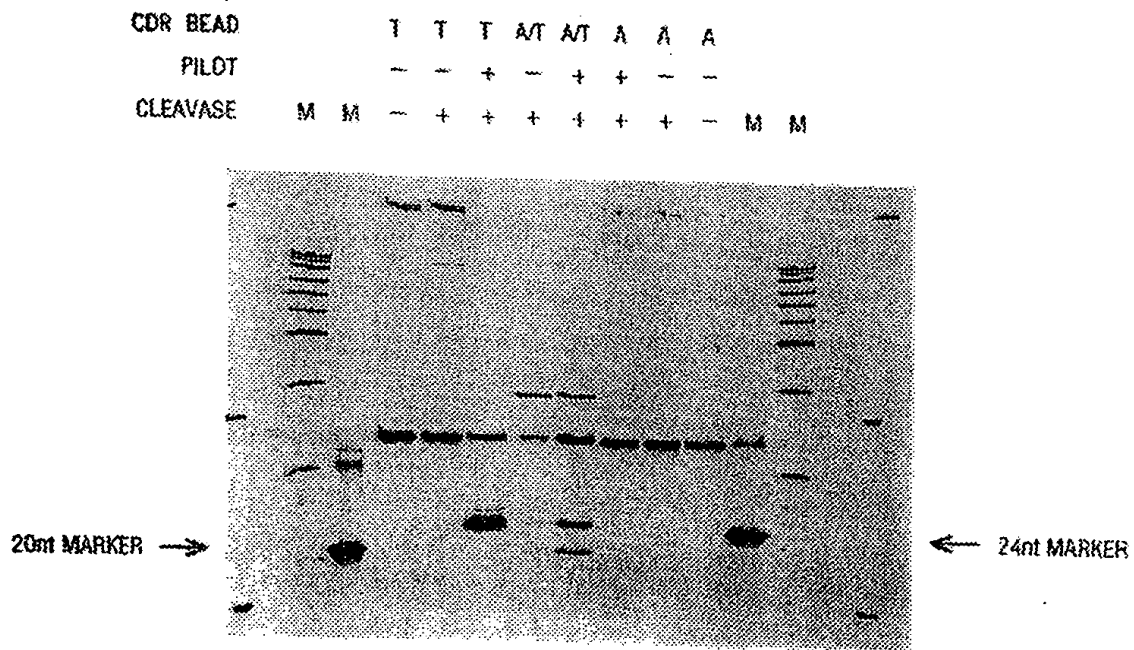


FIG. 24

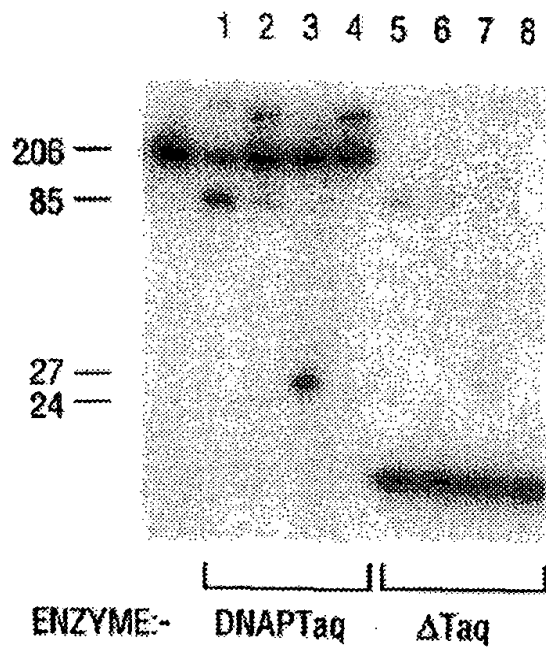


FIG. 25A

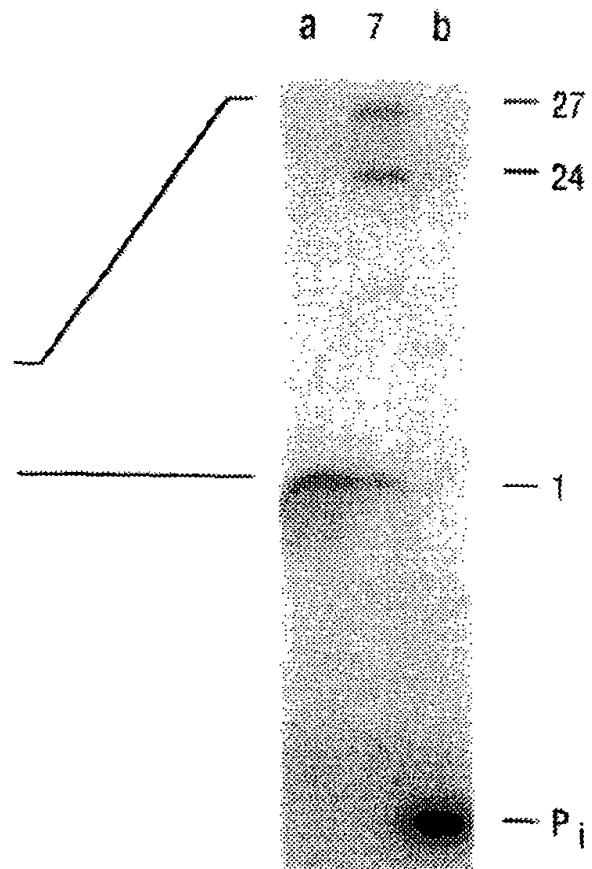


FIG. 25B

FIG. 26A

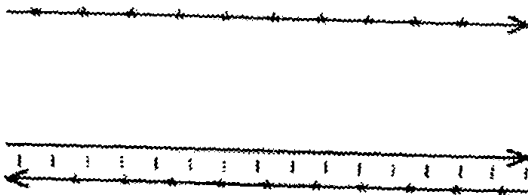
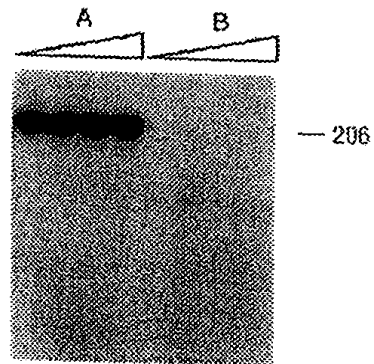


FIG. 26B

$\ast = 32p$



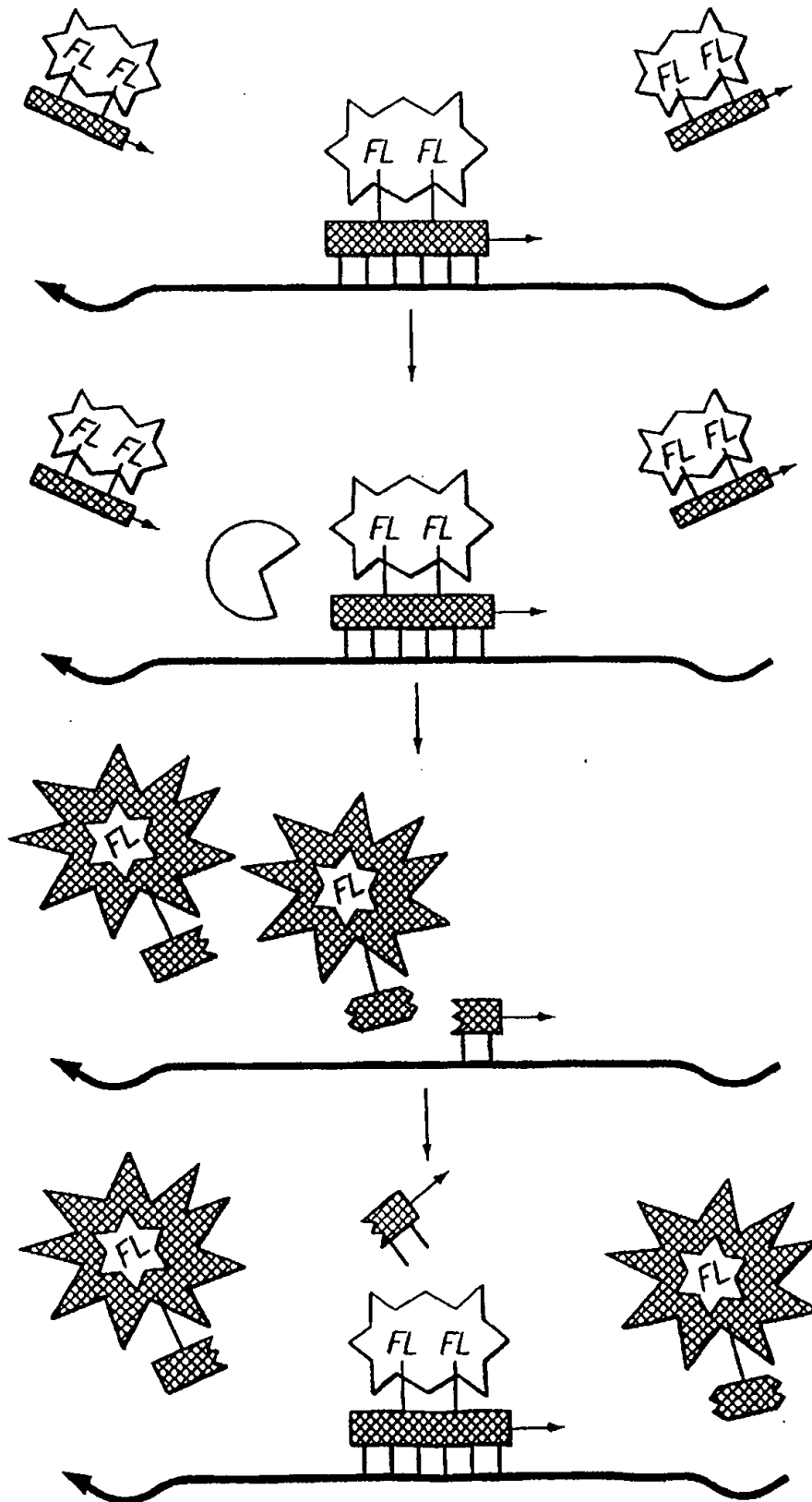
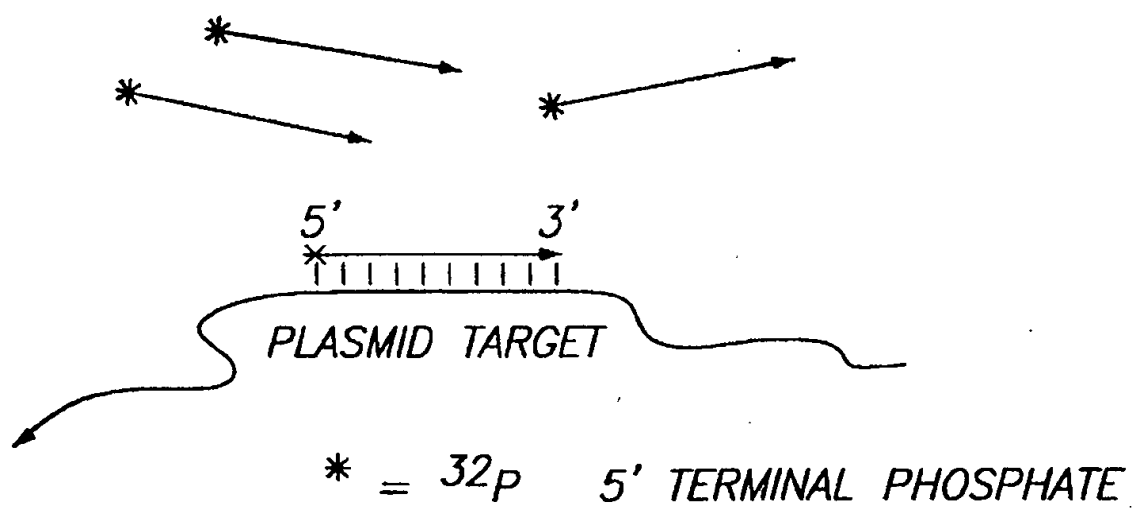
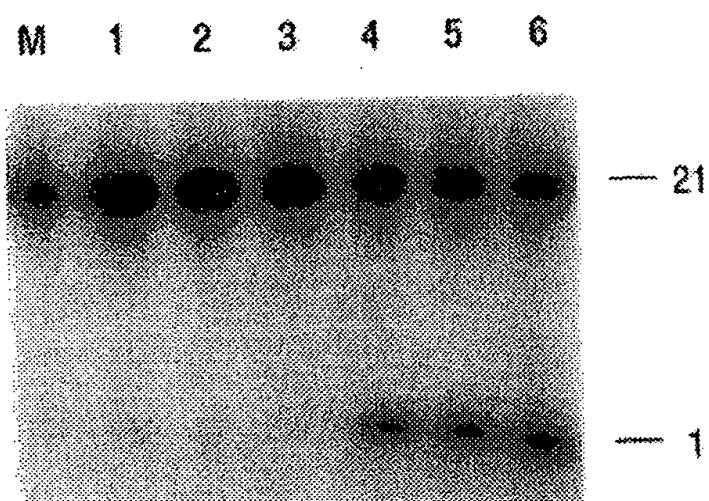
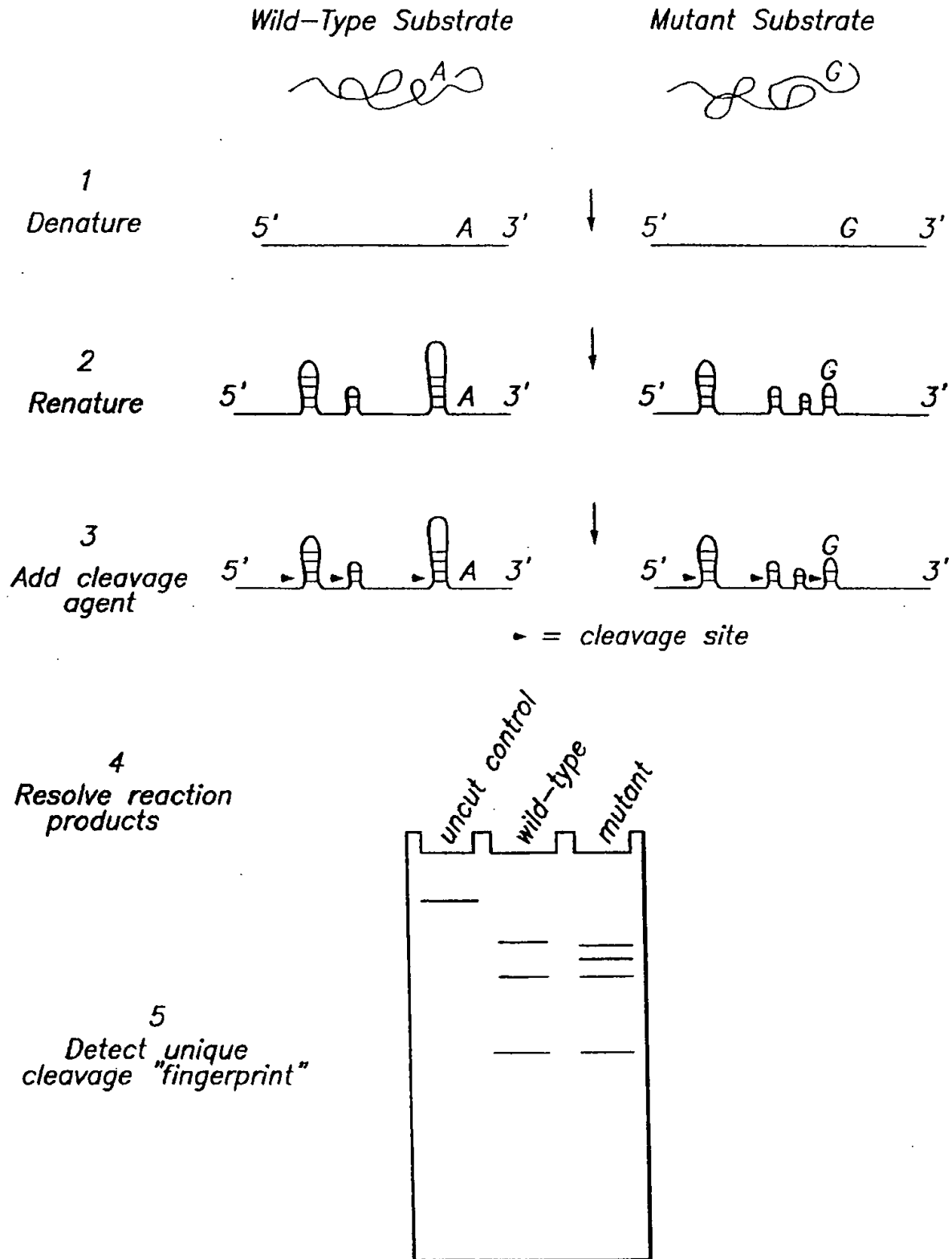


FIG. 27

**FIG. 28A**

**FIG. 28B**

**FIG. 29**

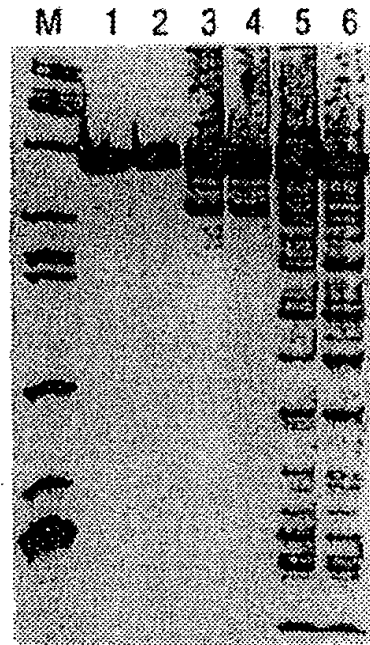


FIG. 30

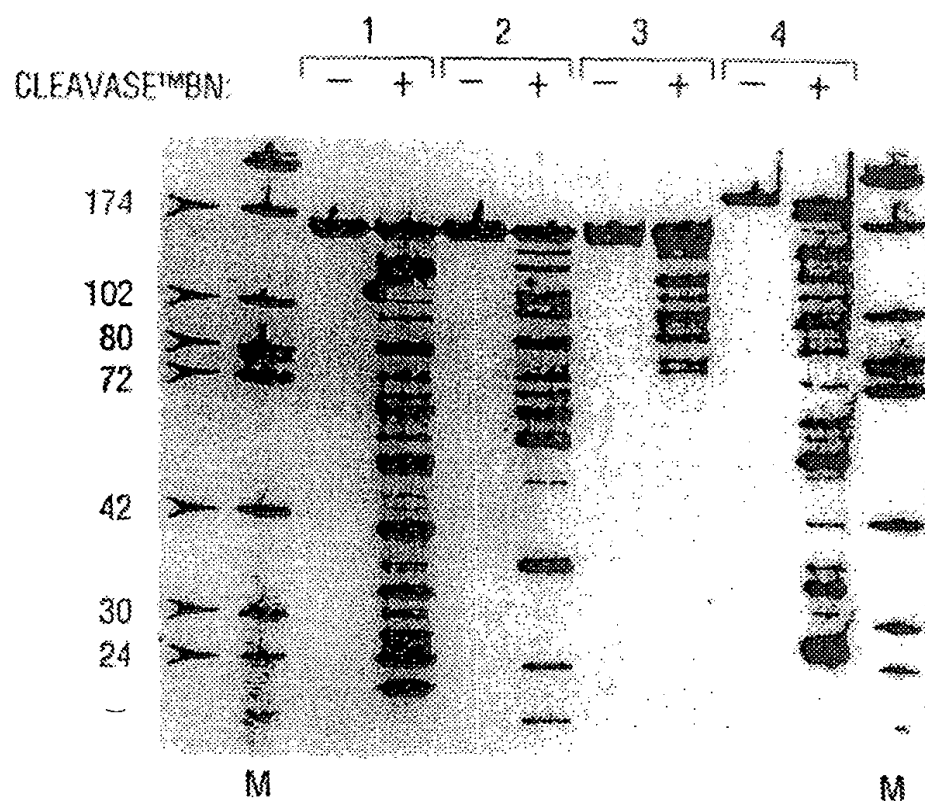


FIG. 31

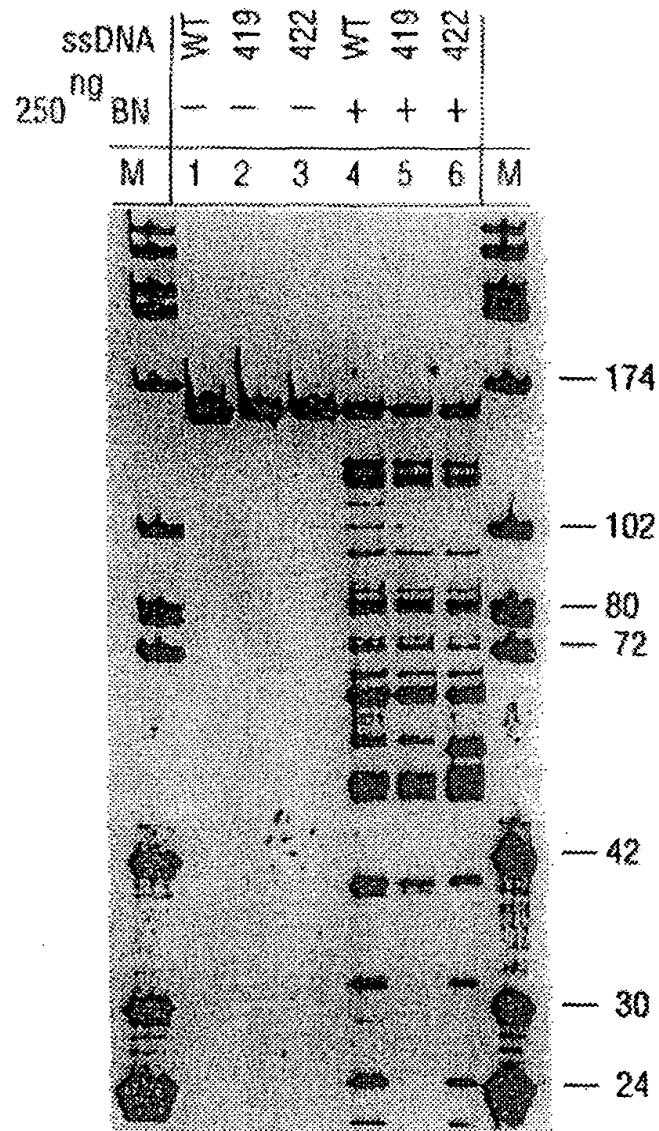
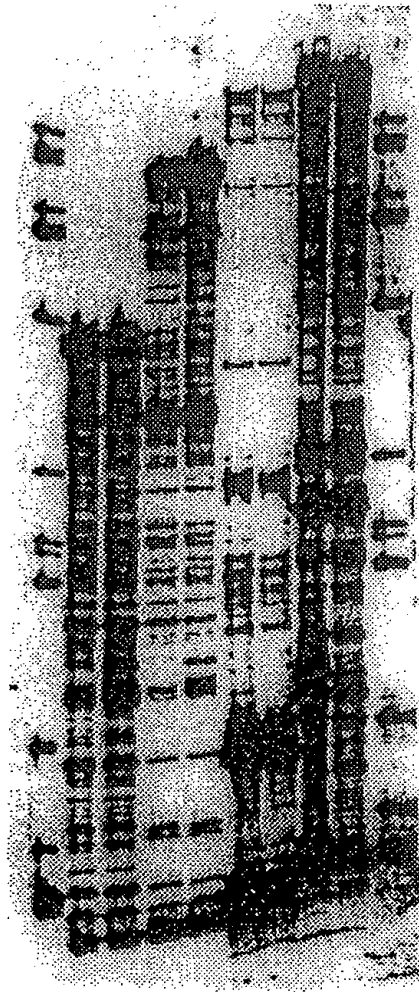


FIG. 32

157 378 1056 1587
M 1 2 3 4 5 6 7 8 M



WT 422 WT 422 WT 422 WT 422

FIG. 33

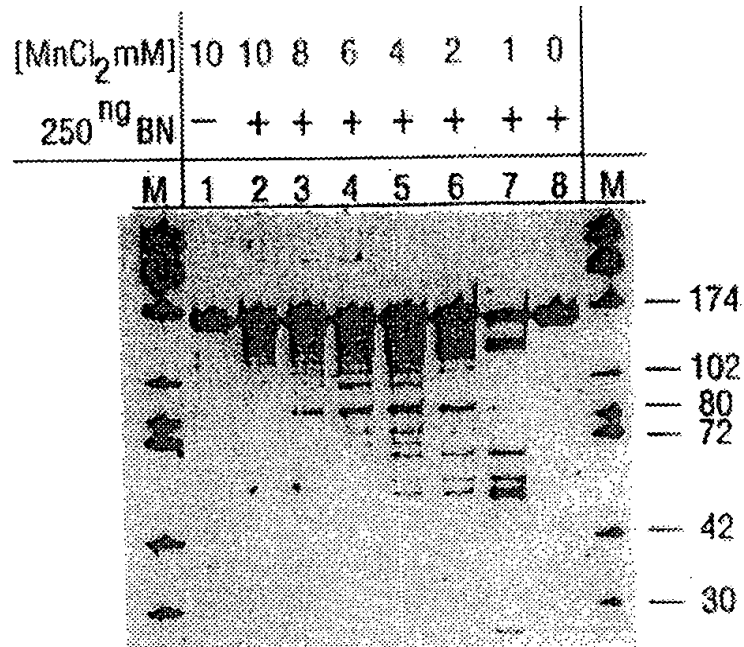


FIG. 34

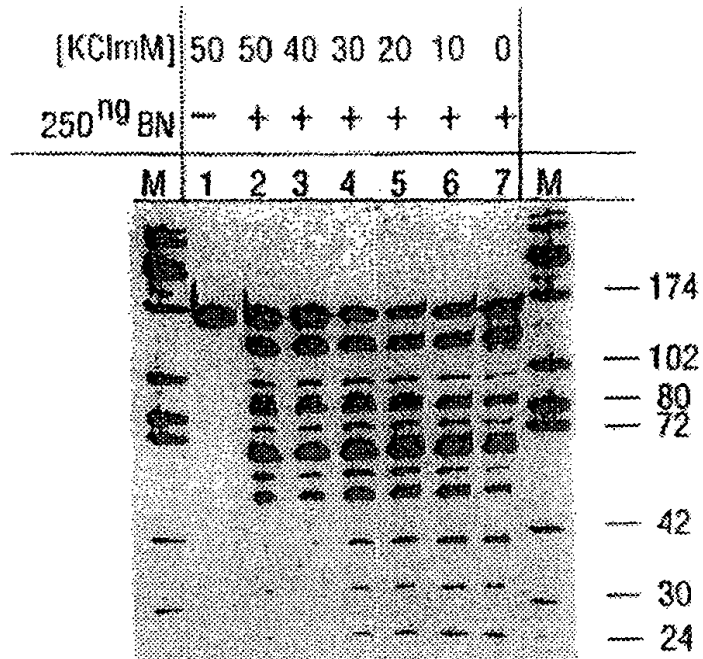


FIG. 35

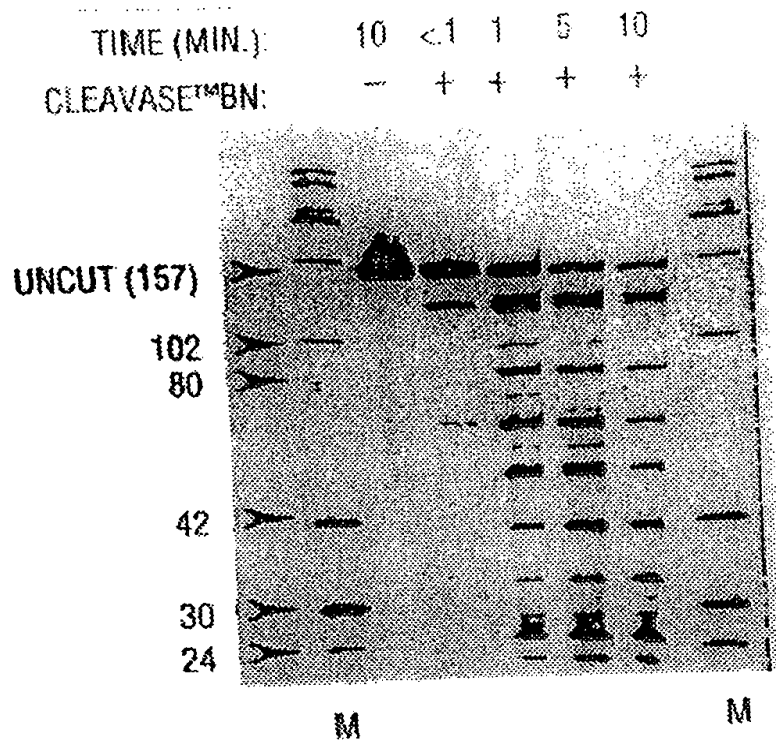


FIG. 36

TEMPERATURE (°C):	55	80	55	60	65	70	75	80
CLEAVASE™BN:	—	—	+	+	+	+	—	+

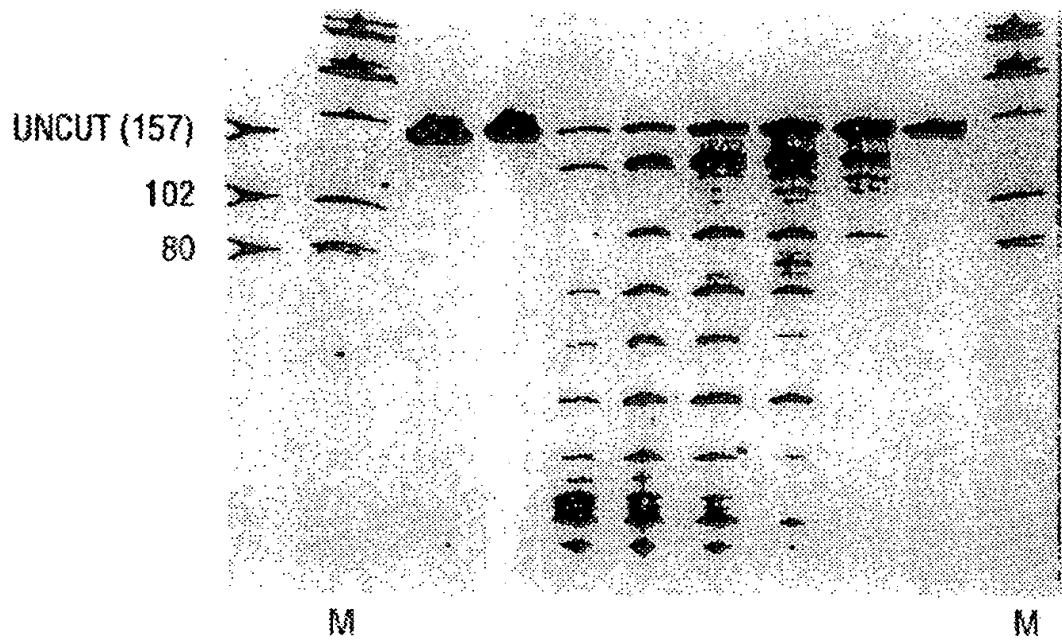


FIG. 37

CLEAVASE™BN (ng): — 10 50 100 250

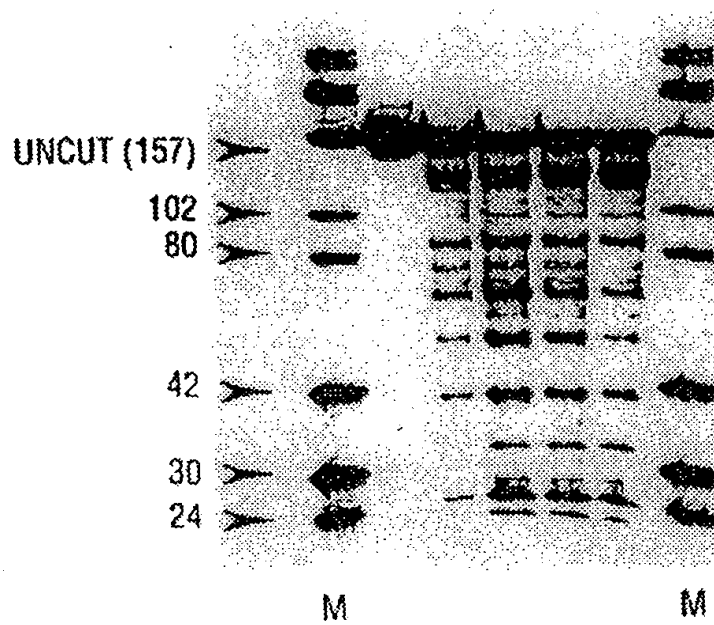


FIG. 38

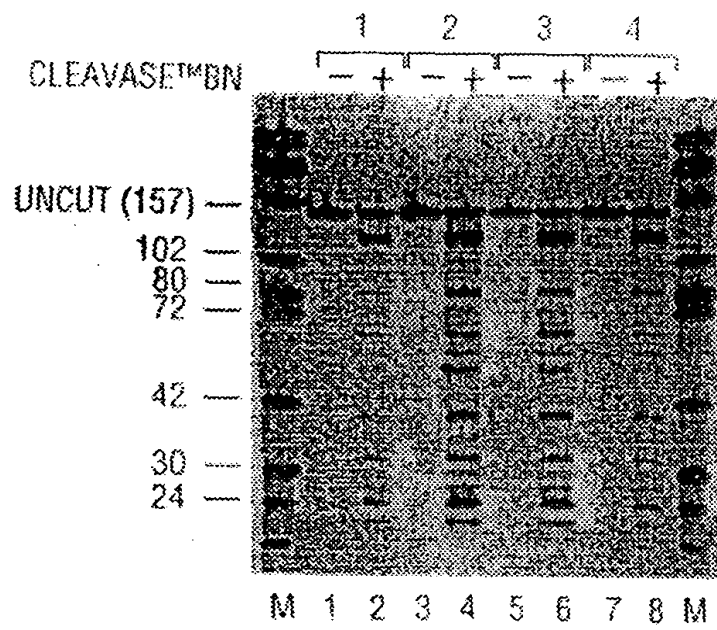


FIG. 39

STRAND	5' - BIOTIN SENSE STRAND						5' - FLUORESCCEIN ANTI-SENSE STRAND					
	WT	419	422	WT	419	422	WT	419	422	WT	419	422
ssDNA	WT	419	422	WT	419	422	WT	419	422	WT	419	422
250 ^{ng} BN	-	-	-	+	+	+	+	+	+	-	-	-
M	1	2	3	4	5	6	7	8	9	10	11	12

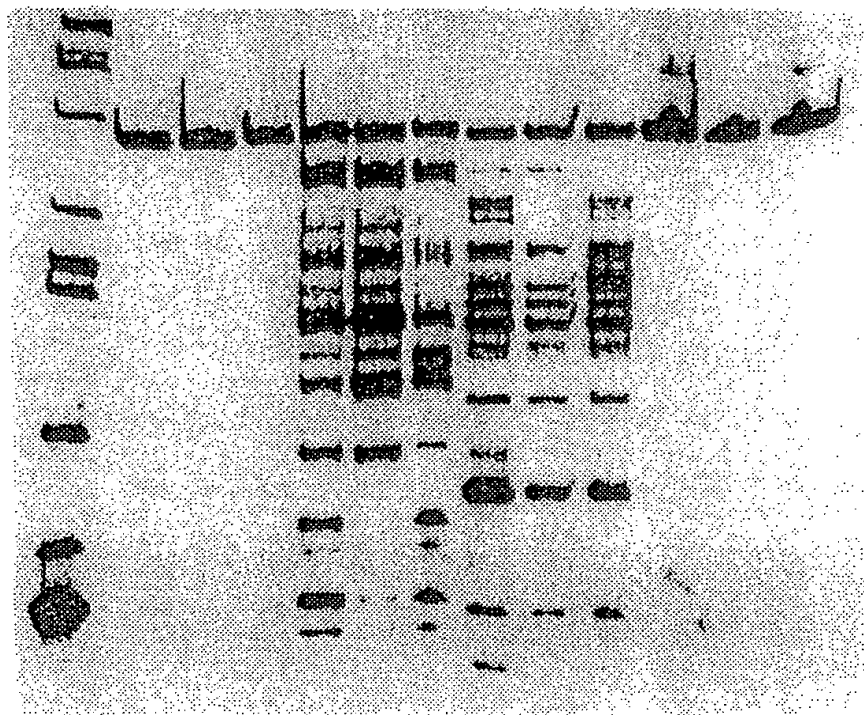


FIG. 40

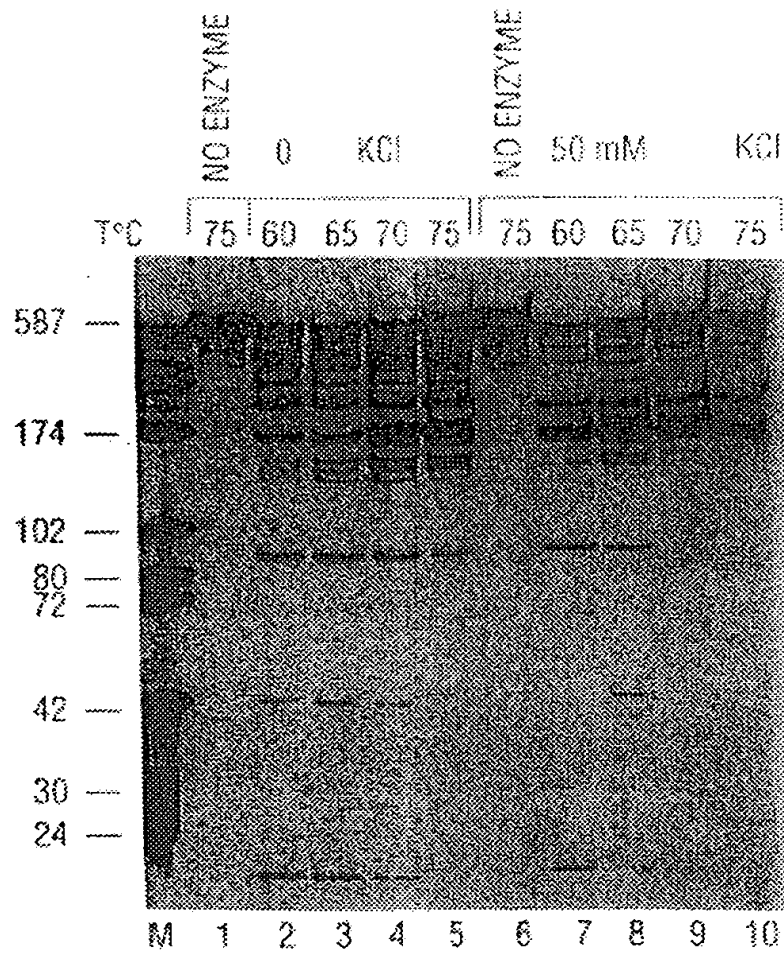


FIG. 41

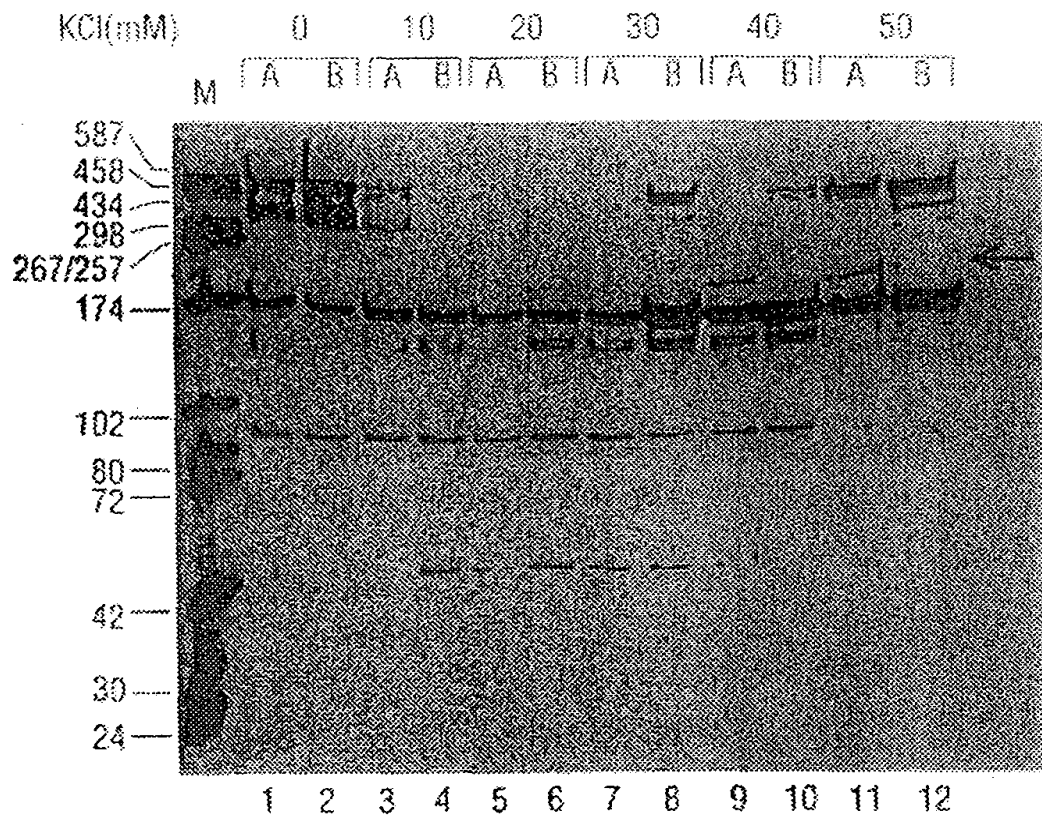


FIG. 42

CLEAVASE™BN

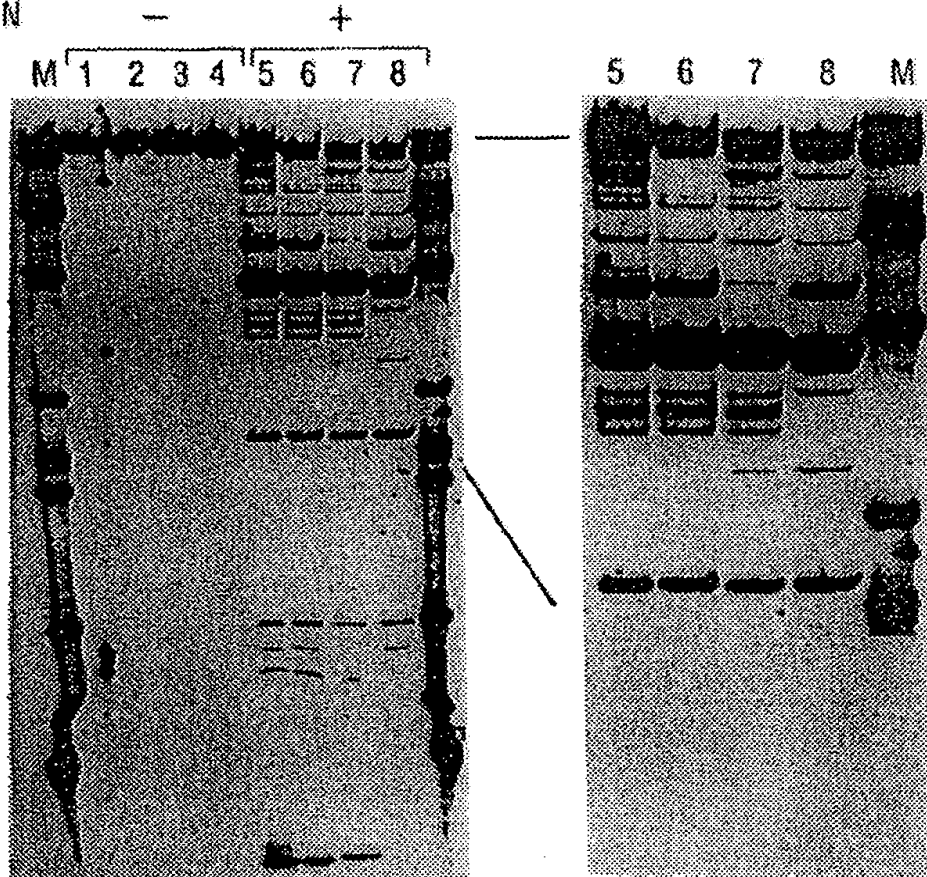


FIG. 43

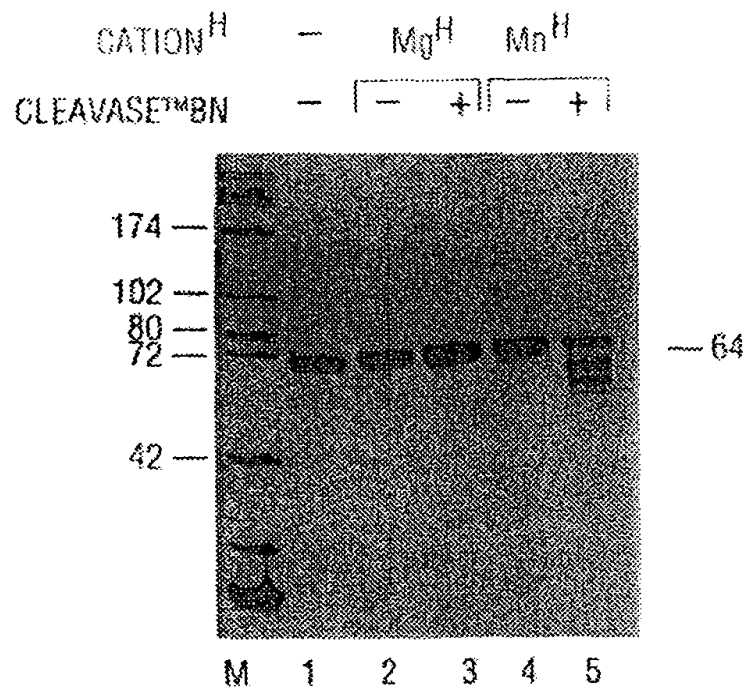


FIG. 44

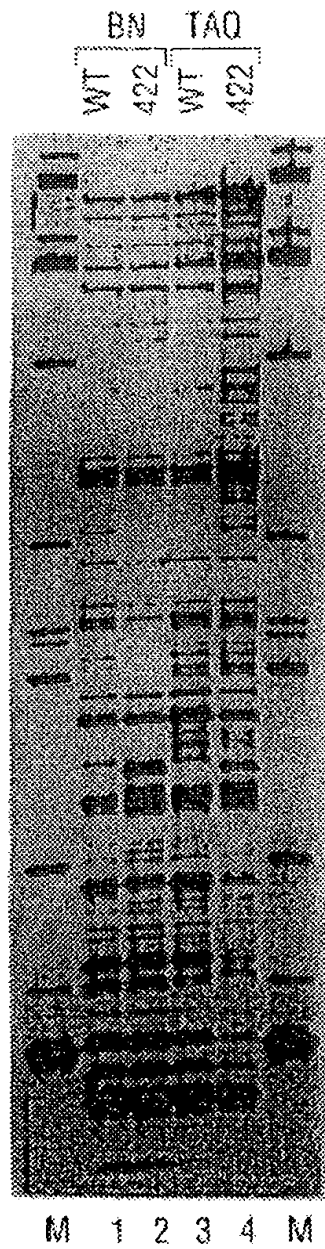


FIG. 45

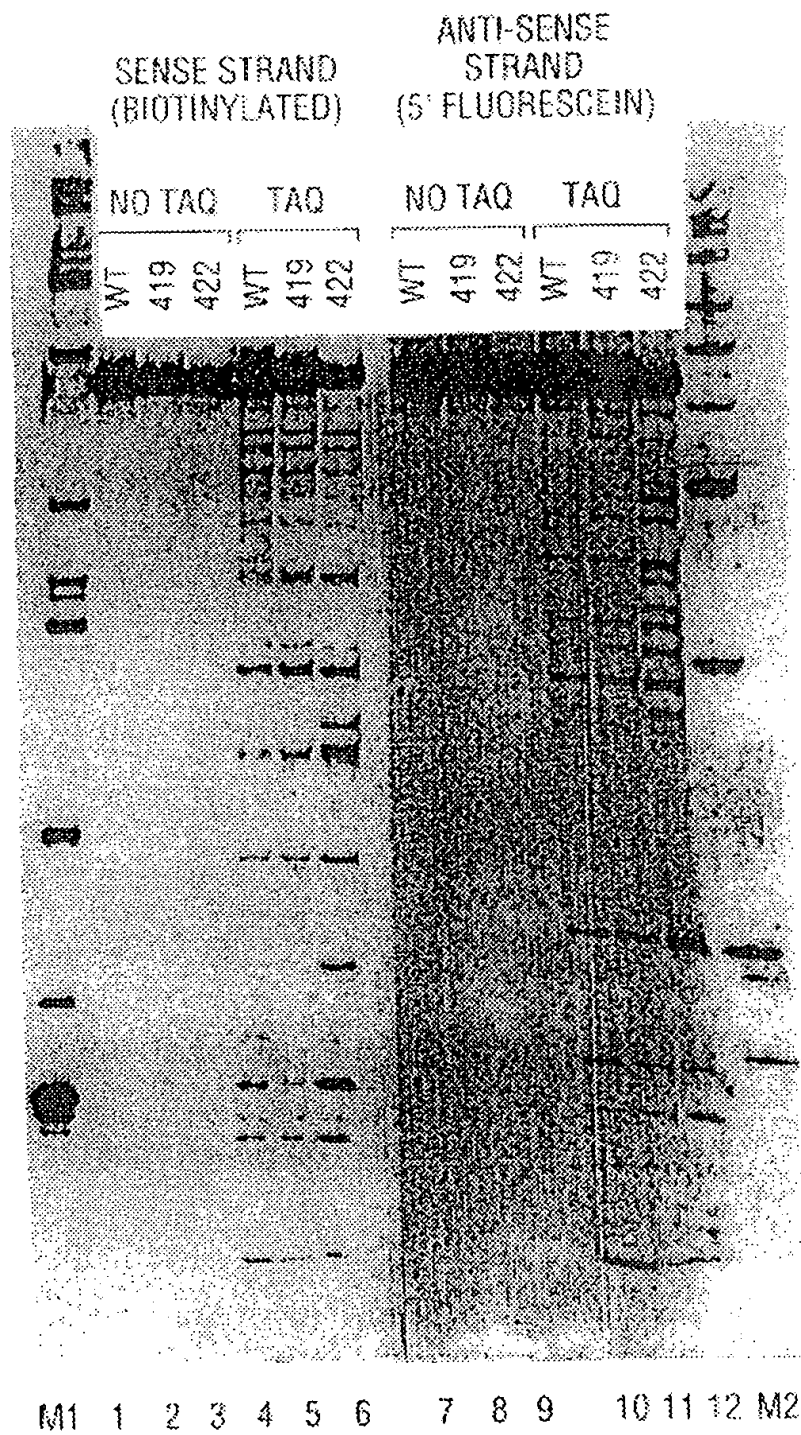


FIG. 46

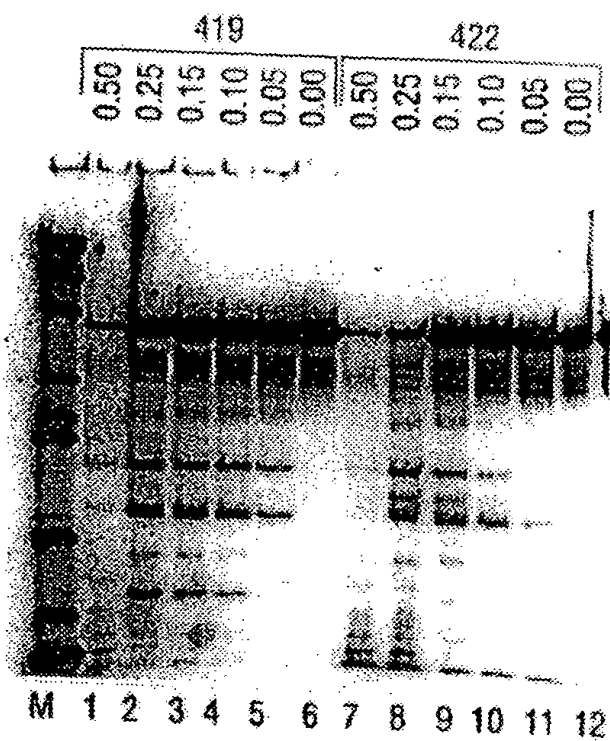


FIG. 47

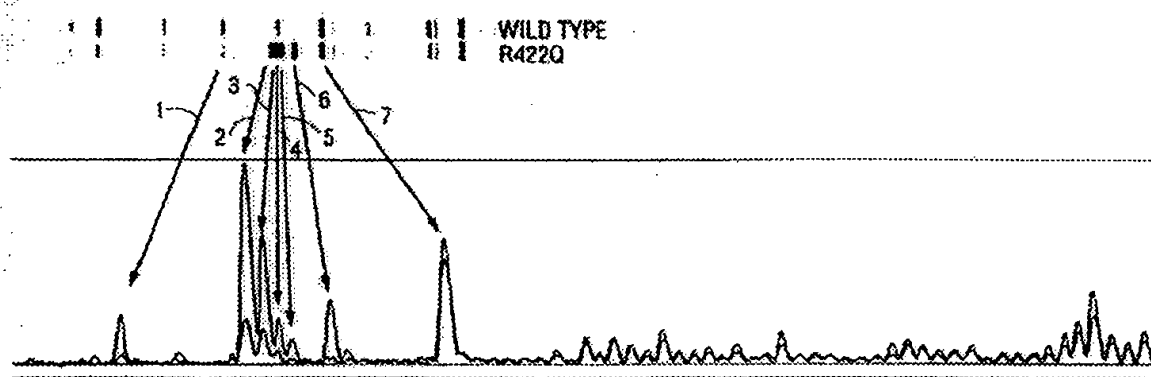


FIG. 48

L.100.8-1		100
(SEQ ID NO: 76)	ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT	
	TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA	
L.46.16-10		
(SEQ ID NO: 77)	ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTTCT	
	TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGGTGAAAGA	
L.46.16-12		
(SEQ ID NO: 78)	ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTTCT	
	TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGGTGAAAGA	
L19.16-3		
(SEQ ID NO: 19)	ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCTCTCT	
	TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGGAGAGA	
L.CEM/251		
(SEQ ID NO: 80)	ATGTTACGGGGAGGTACTGGGAAGGAGCCGGTCGGGAACGCCCACTTTTCT	
	TACAATGCCCCCTCCATGACCCCTTCTCCTCGGCCAGCCCTTGCGGGTGAAAGA	
L.36.8-3		
(SEQ ID NO: 81)	ATGTTACGGGAGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT	
	TACAATGCCCTCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA	

FIG. 49B

Accession	Sequence	Length
L.100.8-1	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA 3'ACTACATATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCT	150
L.46.16-10	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA 3'ACTACATATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCT	
L.46.16-12	5'TGGTGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA 3'ACCACATATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCT	
L.19.16-3	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA 3'ACTACATATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCT	
L.CEM/251	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA 3'ACTACATATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCT	
L.36.8-3	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA 3'ACTACATATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCT	

FIG. 49C

L.100.8-1	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	200
L.46.16-10	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.46.16-12	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.19.16-3	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.CEM/251	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.36.8-3	GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGATCCTCCAAGAGAGGTCGTGATCGTCCATC	

FIG. 49D

09970975 . ON 6 ON

L. 100. 8 -1
(SEQ ID NO: 76)

L. 46.16-10
(SEQ ID NO: 77)

L. 46.16-12
(SEQ ID NO: 78)

L. 19.16-3
(SEQ ID NO: 79)

L. CEM/251
(SEQ ID NO: 80)

L. 36.8-3
(SEQ ID NO: 81)

5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACCTTGGCCGGTGCTGGG

5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACCTTAGCCAGTGCTGGG

5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACCTTGGCCAGTGCTGGG

5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACCTTGGCCGGTGCTGGG

5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACCTTGGCCGGTGCTGGG

5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACCTTGGCCGGTGCTGGG

5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACCTTGGCCGGTGCTGGG

5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACCTTGGCCGGTGCTGGG

3'TCGGACCCACAAAGGACCATCTGAGAGTGGTCGTGAACCGGCCACGACCC

3'TCGGACCCACAAAGGACGATCTGAGAGTGGTCGTGAATCGGTCACGACCC

3'TCGGACCCACAAAGGACGATCTGAGAGTGGTCGTGAACCGGTCACGACCC

3'TCGGACCCACAAAGGACGATCTGAGAGTGGTCGTGAACCGGCCACGACCC

3'TCGGACCCACAAAGGACGATCTGAGAGTGGTCGTGAACCGGCCACGACCC

3'TCGGACCCACAAAGGACGATCTGAGAGTGGTCGTGAACCGGCCACGACCC

3'TCGGACCCACAAAGGACGATCTGAGAGTGGTCGTGAACCGGCCACGACCC

3'TCGGACTCACAAGGACGATTTGAGAGTGGTCGTGAACCGGCCACGACCC

250

HAIRPIN

FIG. 49E

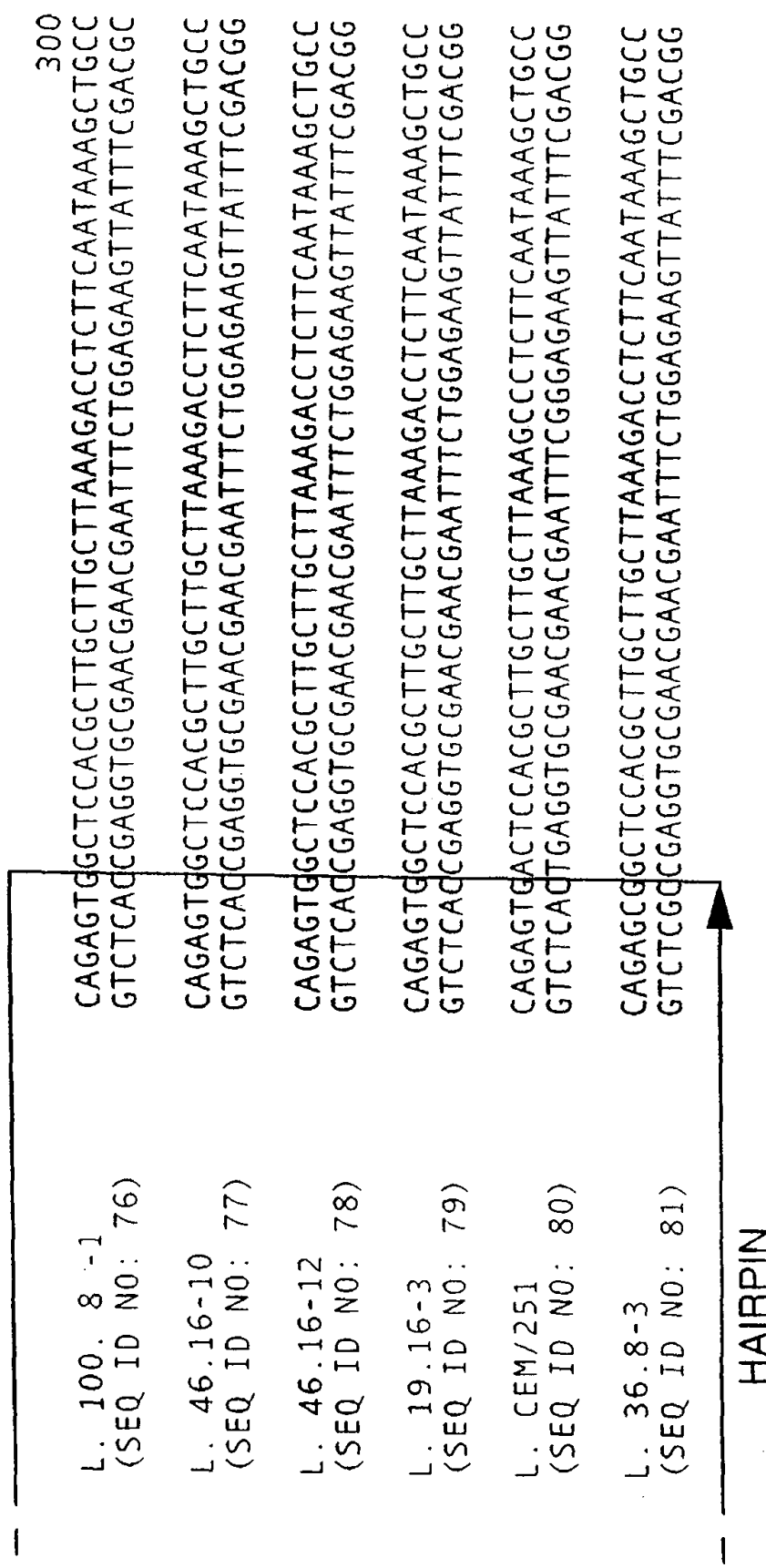


FIG. 49F

350

L.100.8-1	5'ATTTTAGAAGTAGGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3'
	3'TAAATCTTCAATCCGGTCACACACAAGGGTAGAGGATCGGCGCGGAC C 5'
L.46.16-10	5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3'
	3'TAAATCTTCAATCCGGTCACACACAAGGGTAGAGGATCGGCGCGGAC C 5'
L.46.16-12	5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3'
	3'TAAATCTTCAATCCGGTCACACACAAGGGTAGAGGATCGGCGCGGAC C 5'
L.19.16-3	5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3'
	3'TAAATCTTCAATCCGATCACACACAAGGGTAGAGGATCGGCGCGGAC C 5'
L.CEM/251	5'ATTTTAGAAGTAAGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3'
	3'TAAATCTTCAATCCGATCACACACAAGGGTAGAGGATCGGCGCGGAC C 5'
L.36.8-3	5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3'
	3'TAAATCTTCAATCCGATCACACACAAGGGTAGAGGATCGGCGCGGAC C 5'

FIG. 49G

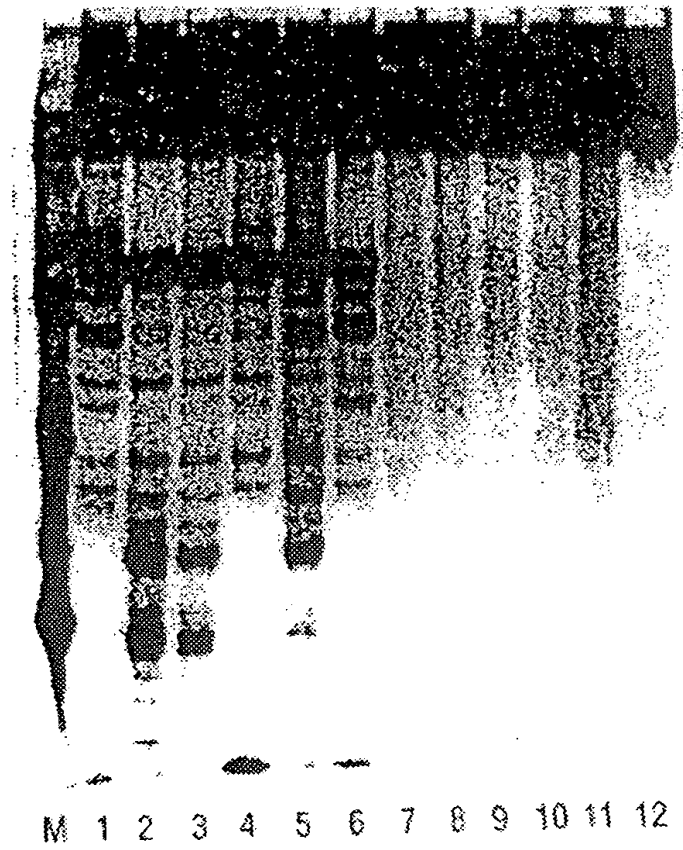


FIG. 50

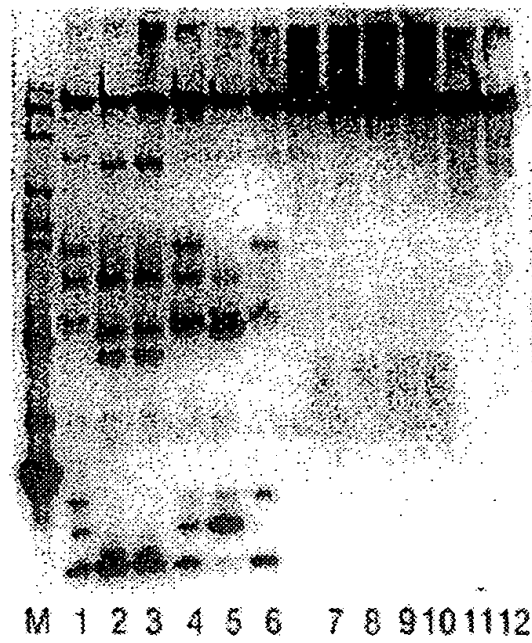


FIG. 51

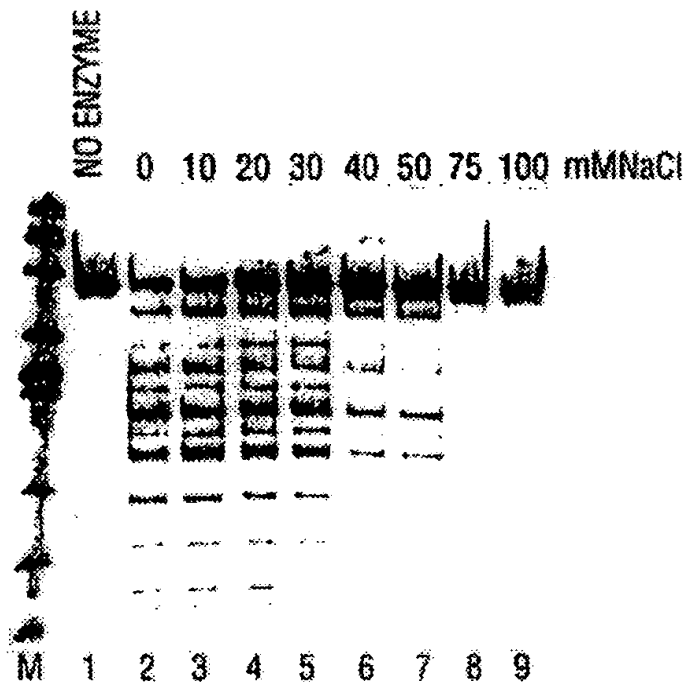


FIG. 52

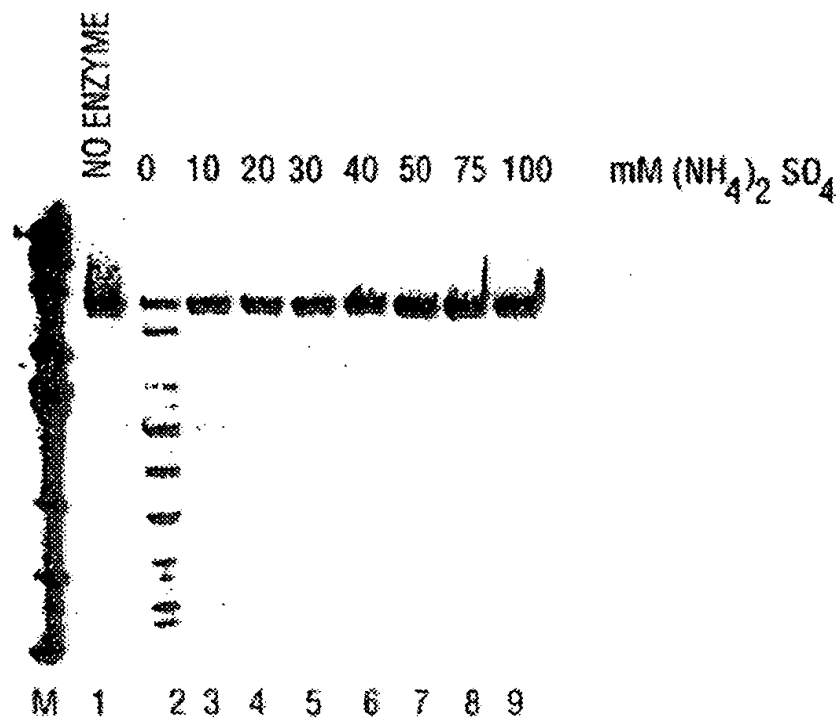


FIG. 53

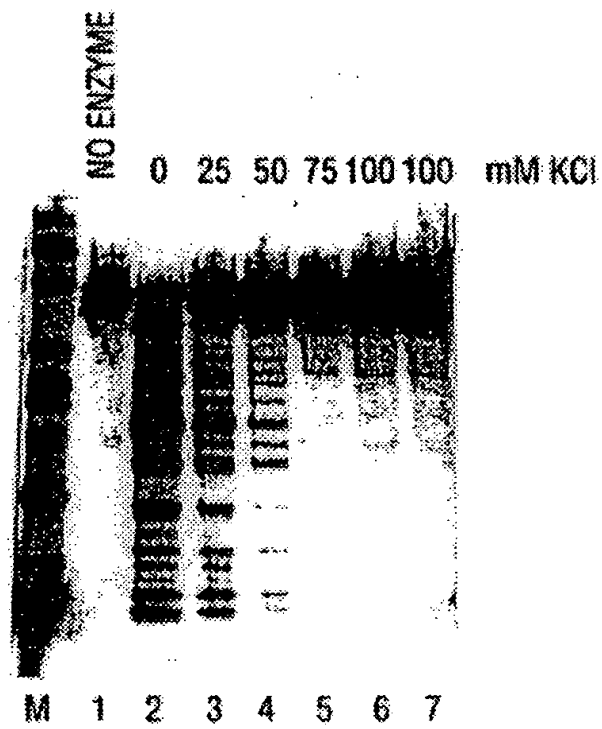


FIG. 54

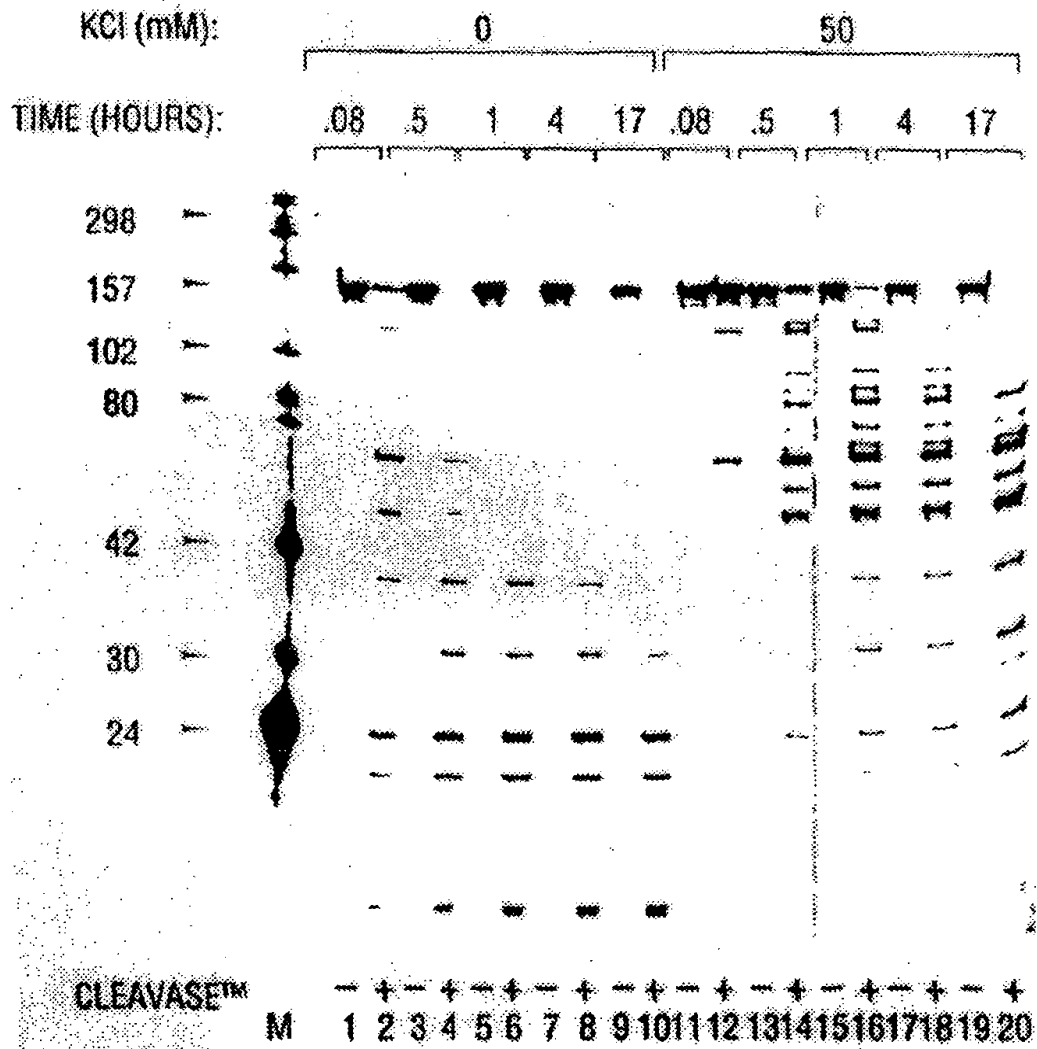


FIG. 55

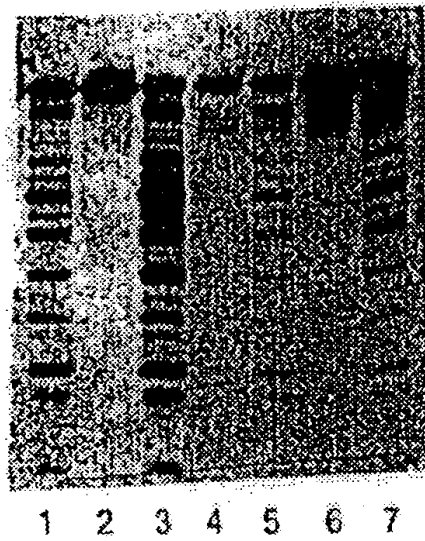


FIG. 56

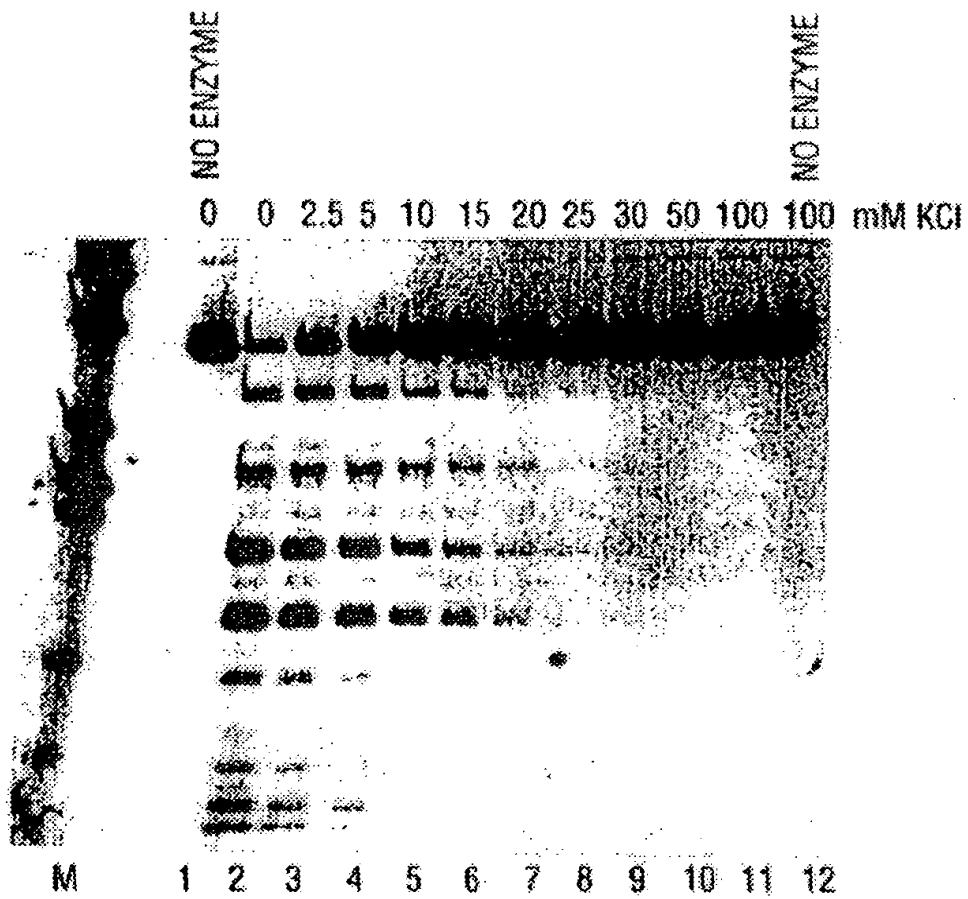


FIG. 57

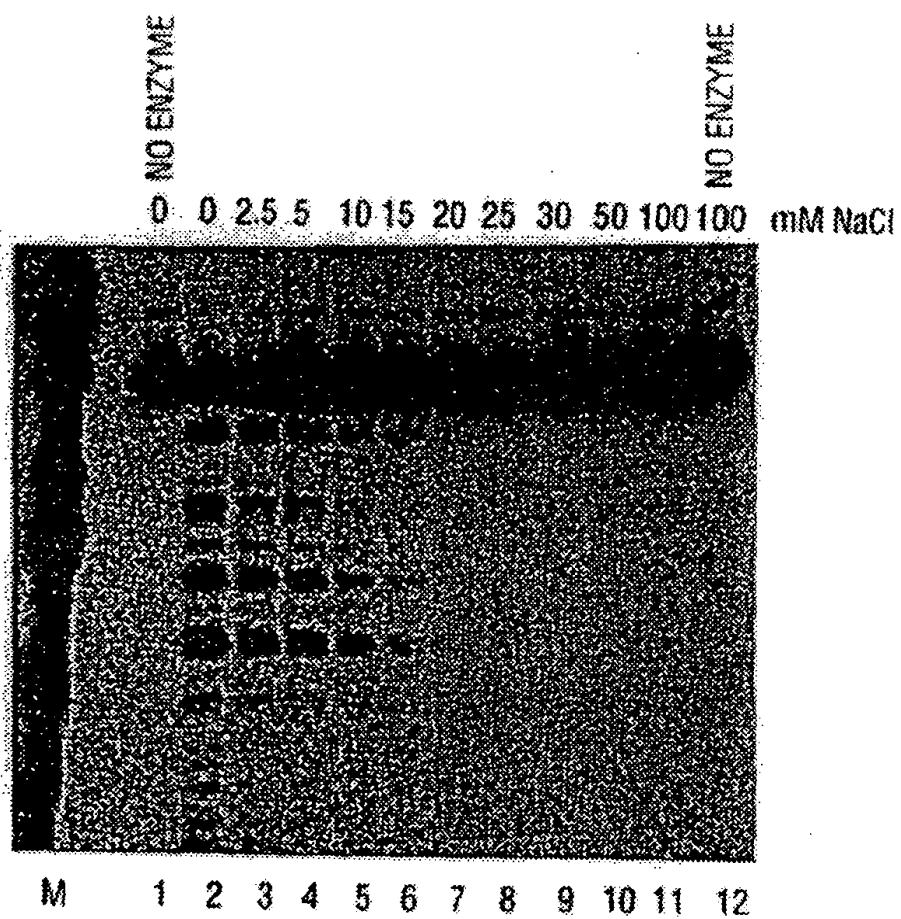


FIG. 58

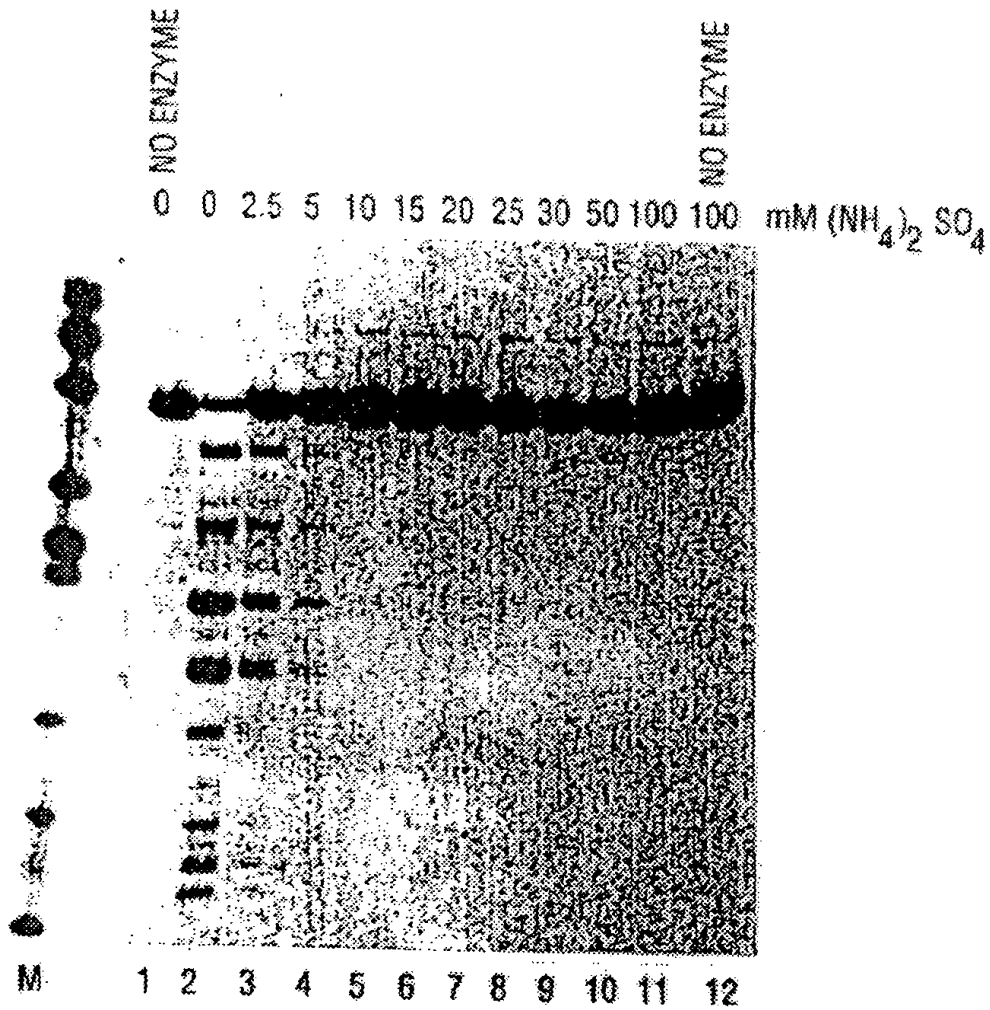


FIG. 59

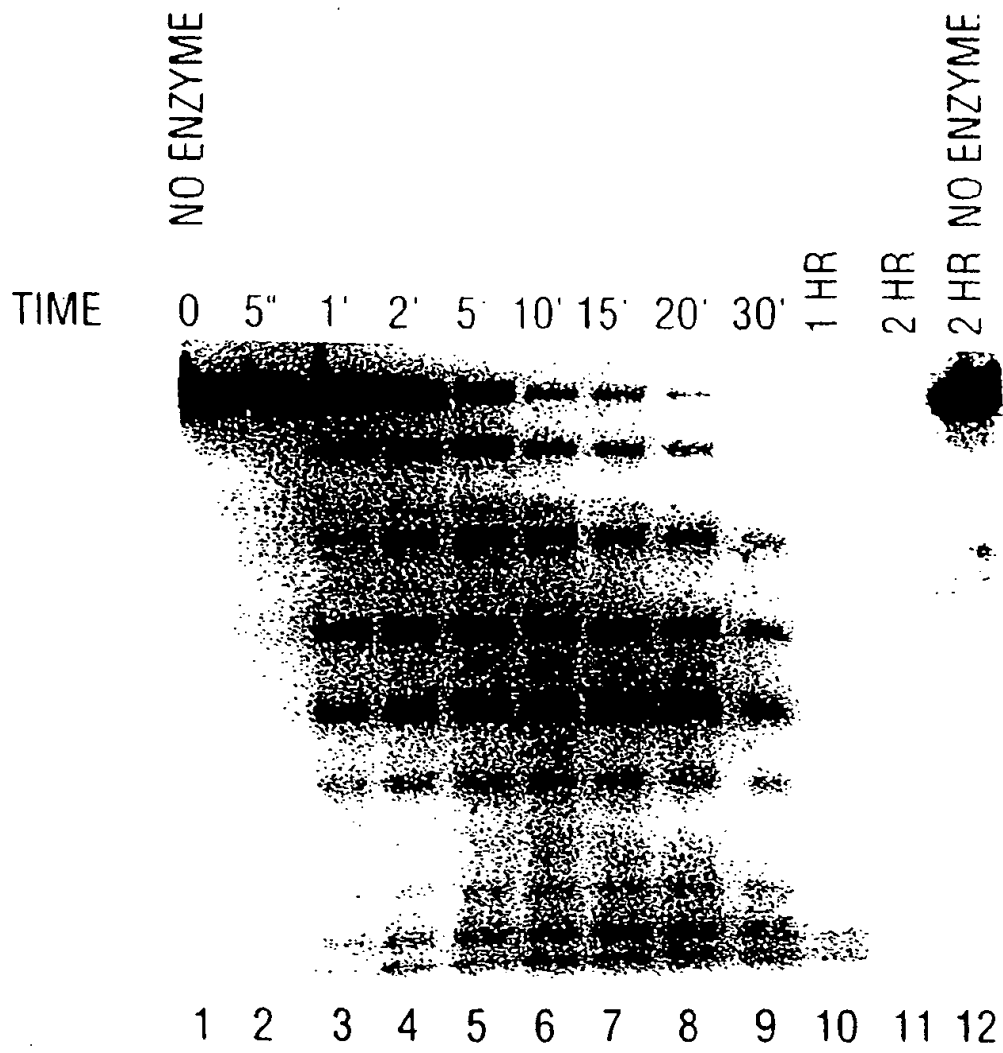


FIG. 60

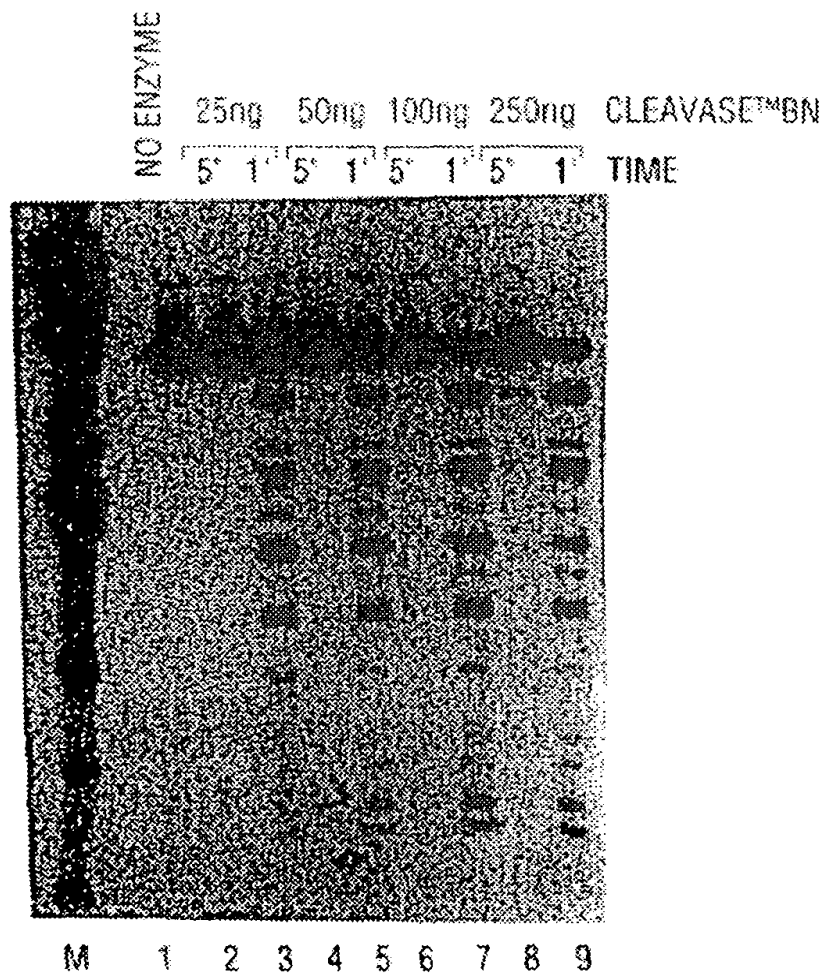


FIG. 61

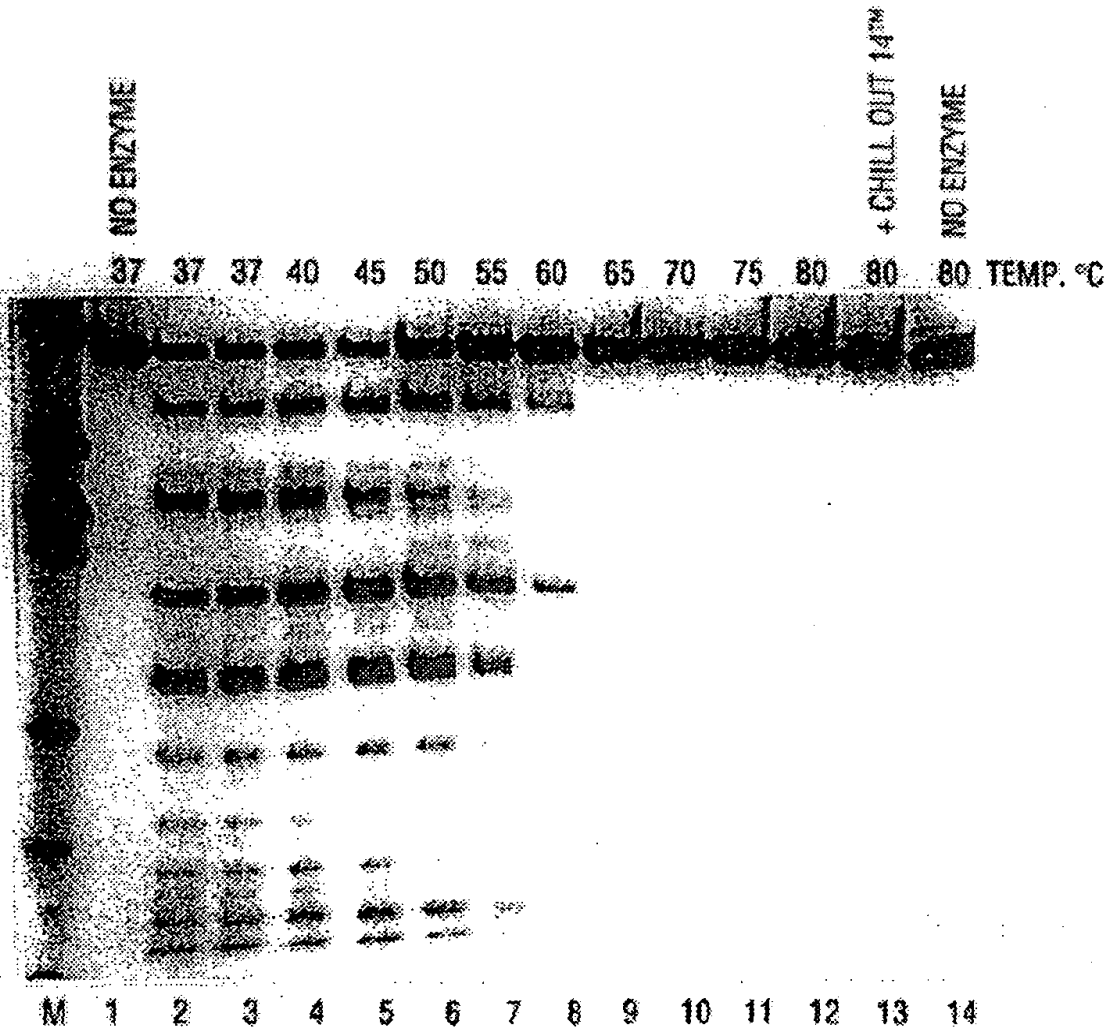


FIG. 62

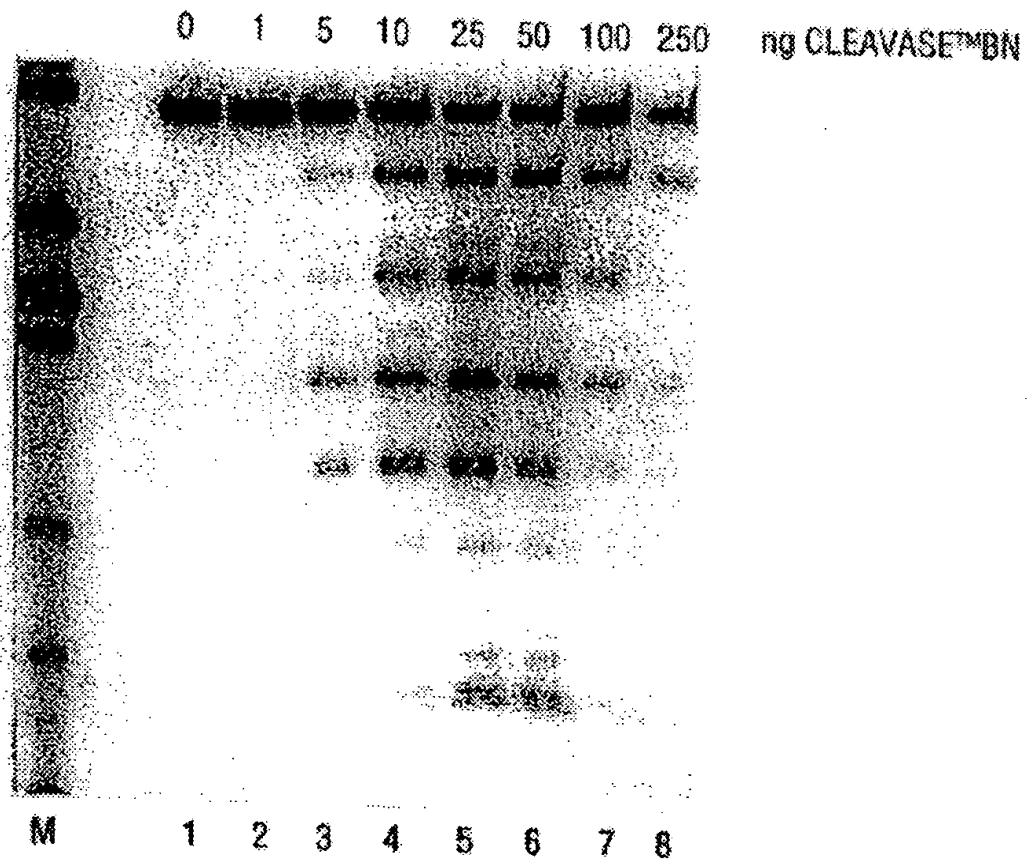


FIG. 63

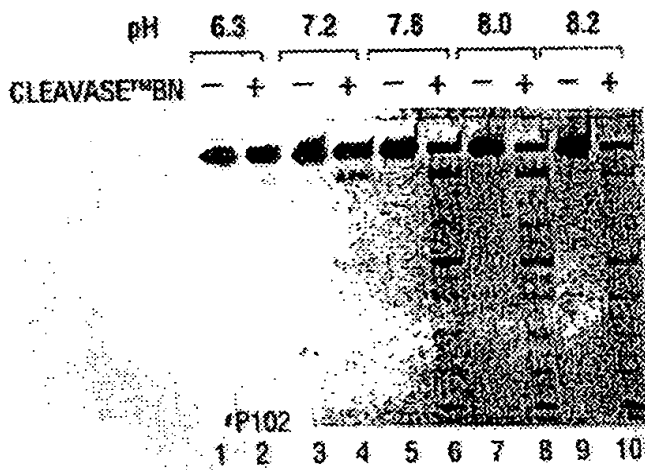


FIG. 64A

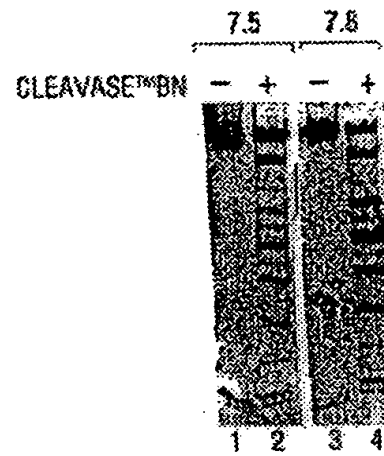


FIG. 64B

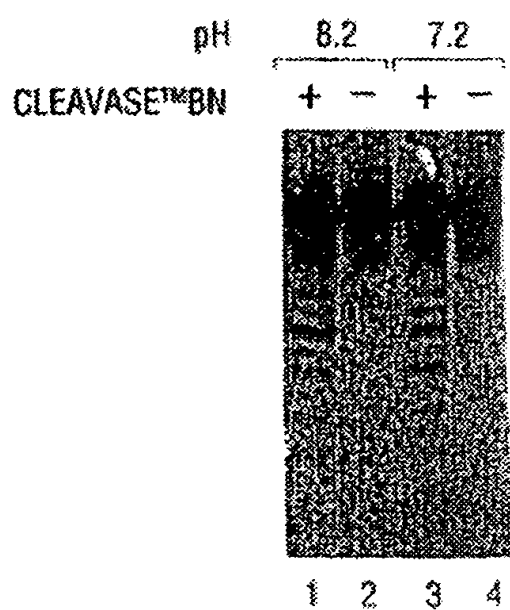


FIG. 65A

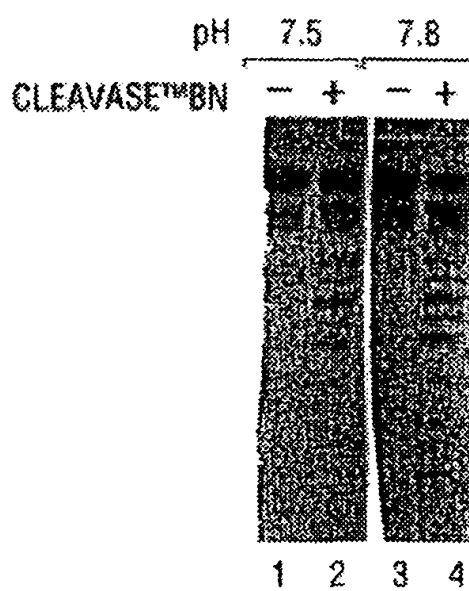


FIG. 65B

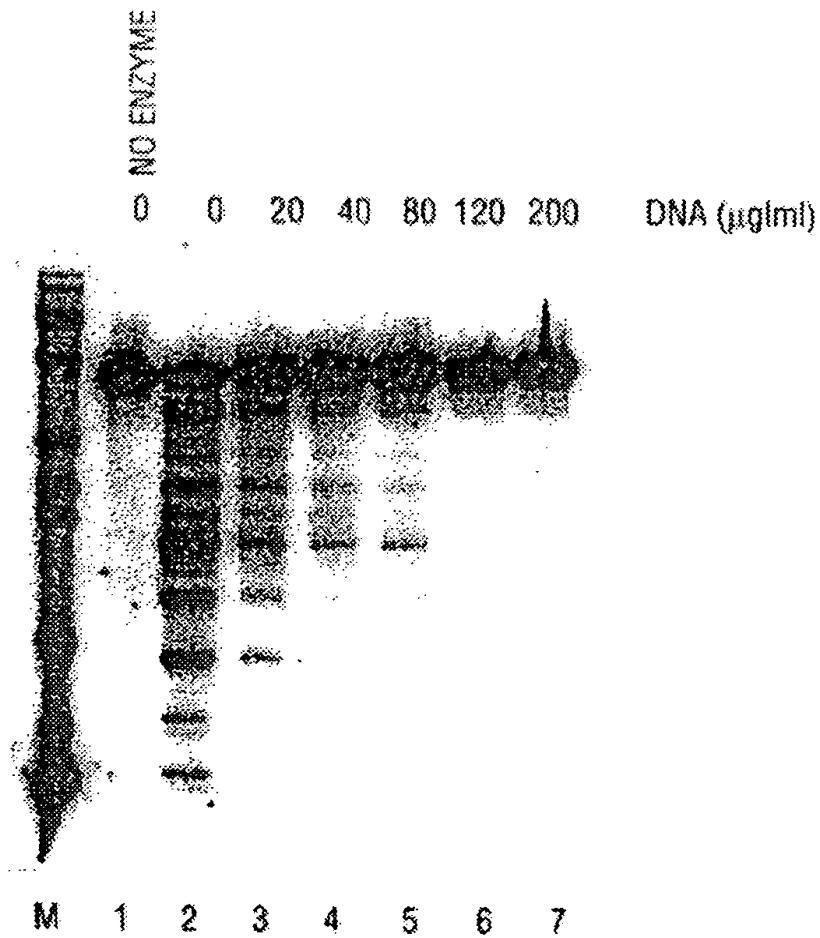


FIG. 66

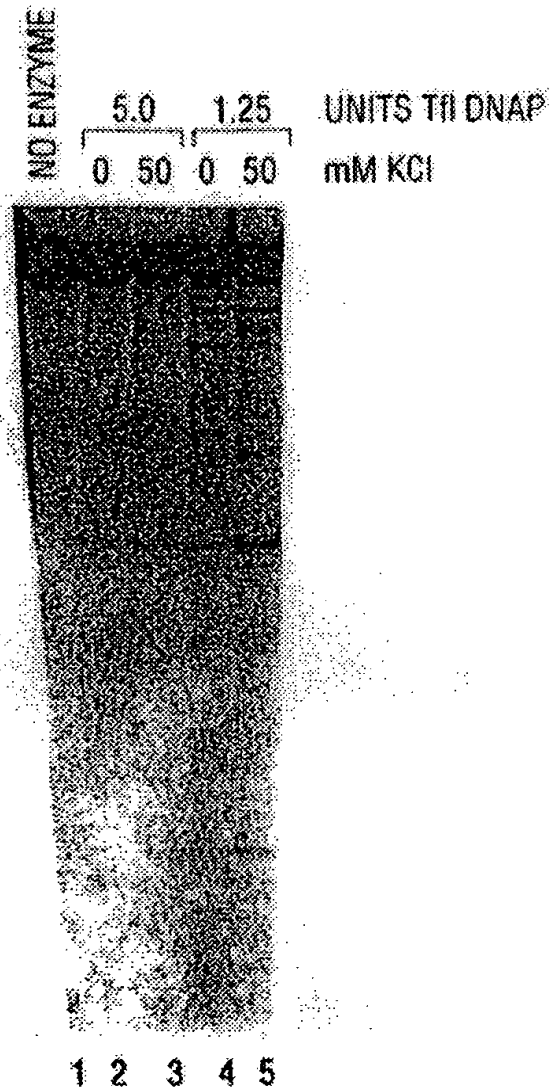


FIG. 67

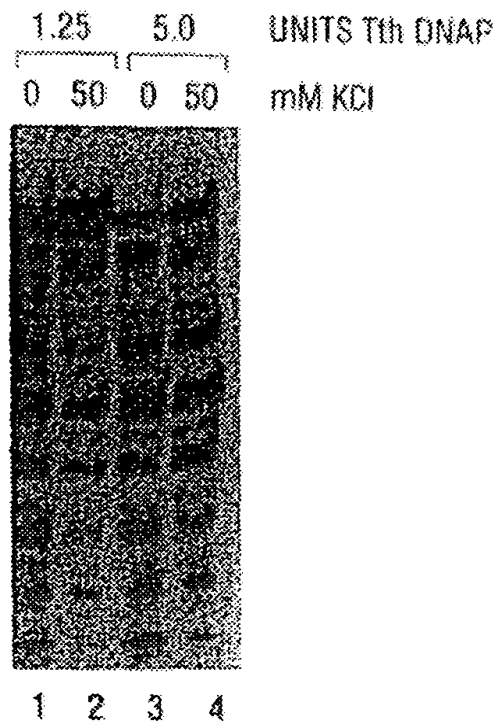


FIG. 68

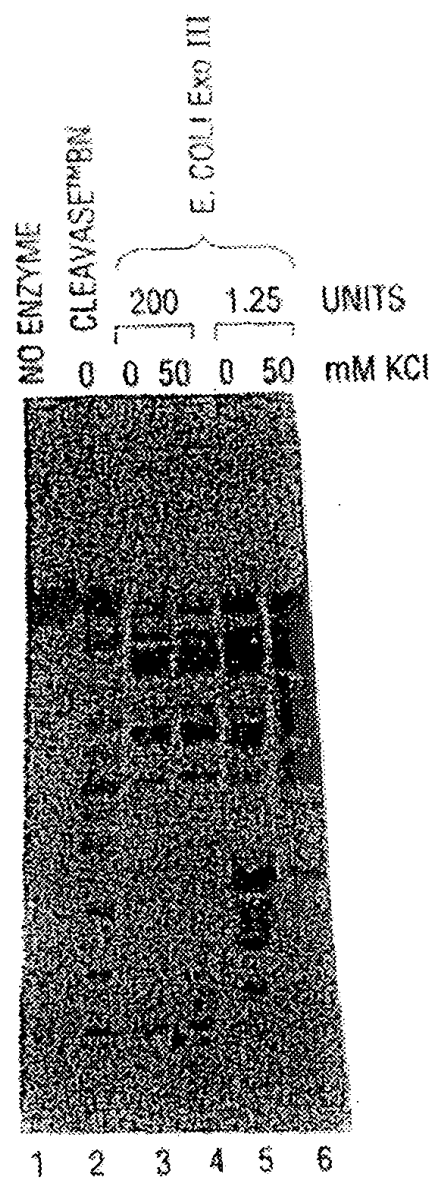


FIG. 69

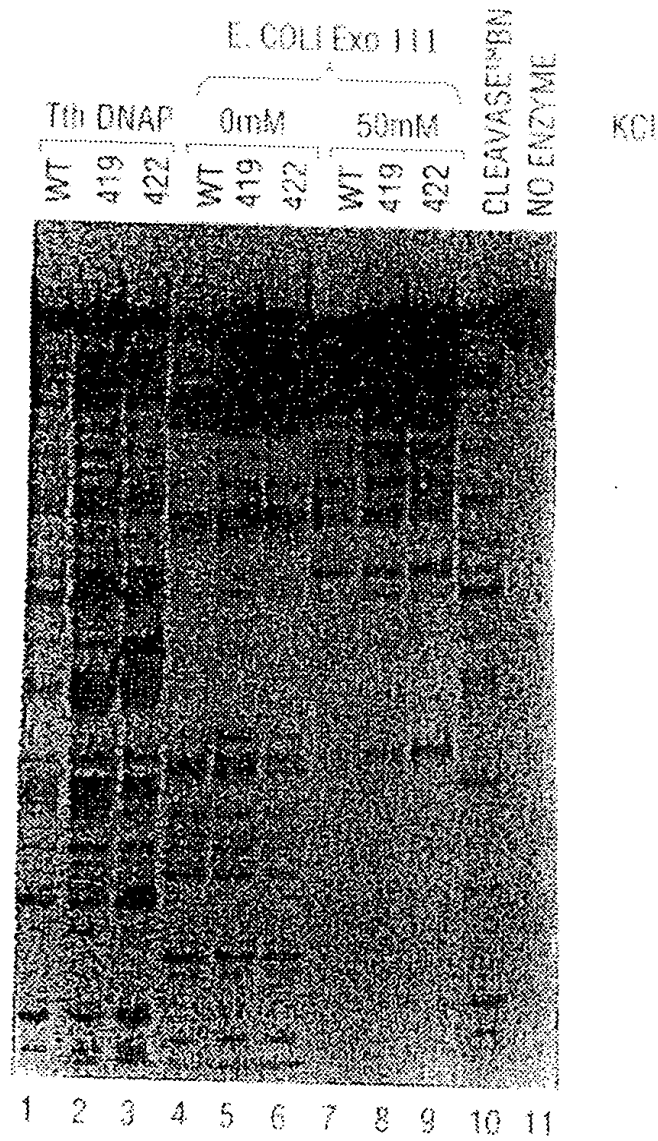
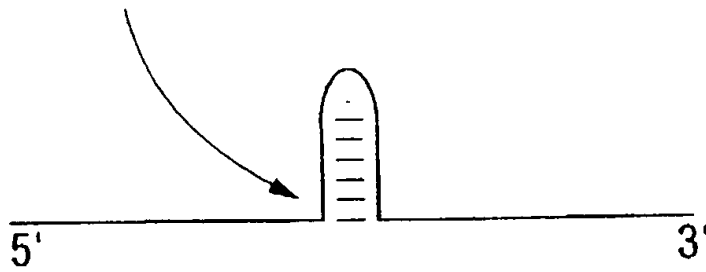


FIG. 70

5' CLEAVAGE SITE



3' CLEAVAGE SITE

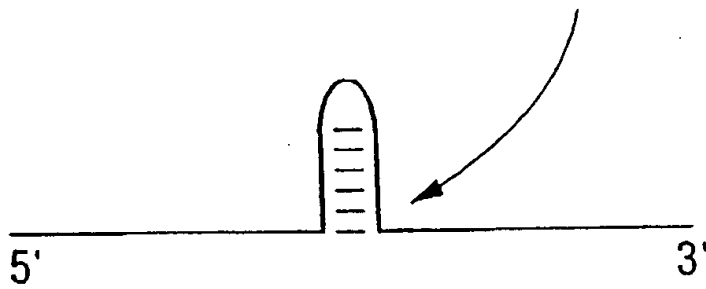


FIG. 71

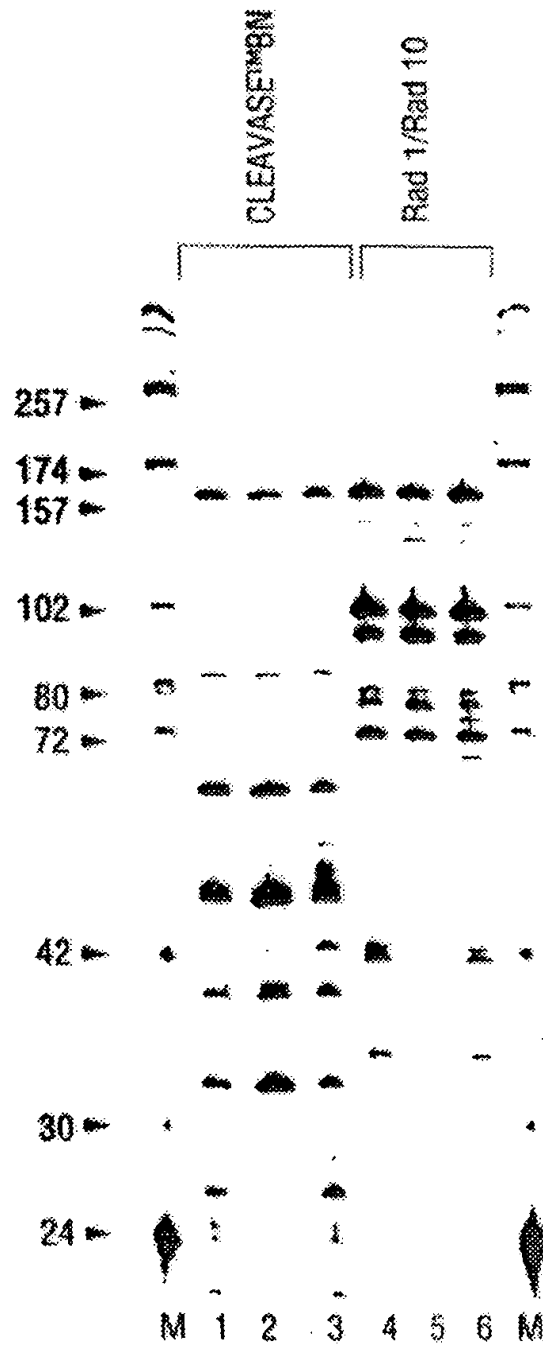


FIG. 72

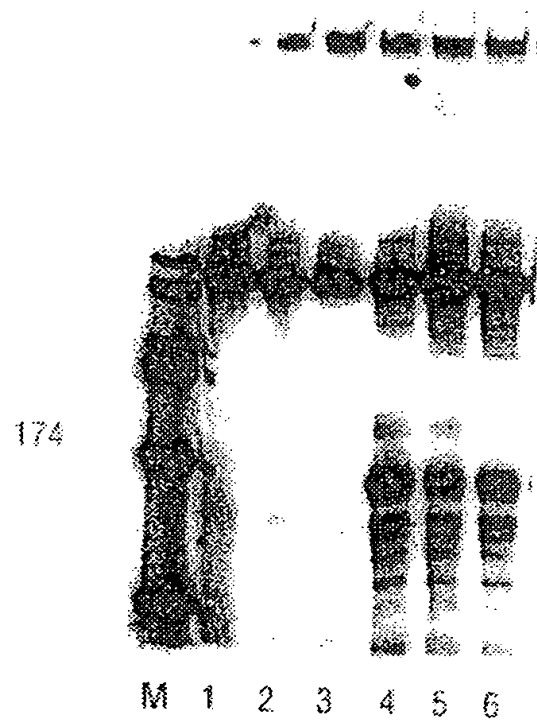


FIG. 73

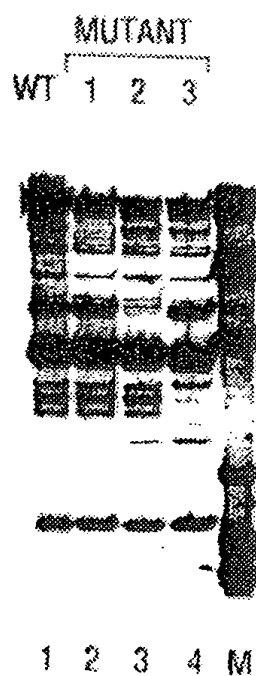


FIG. 74A

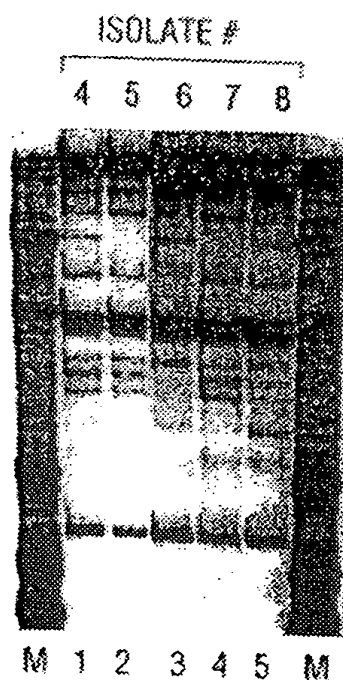


FIG. 74B

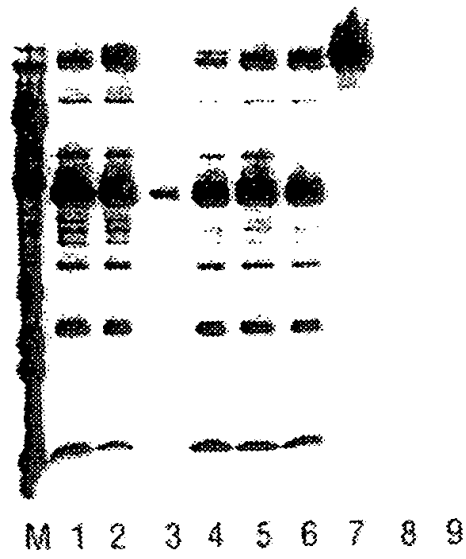


FIG. 75

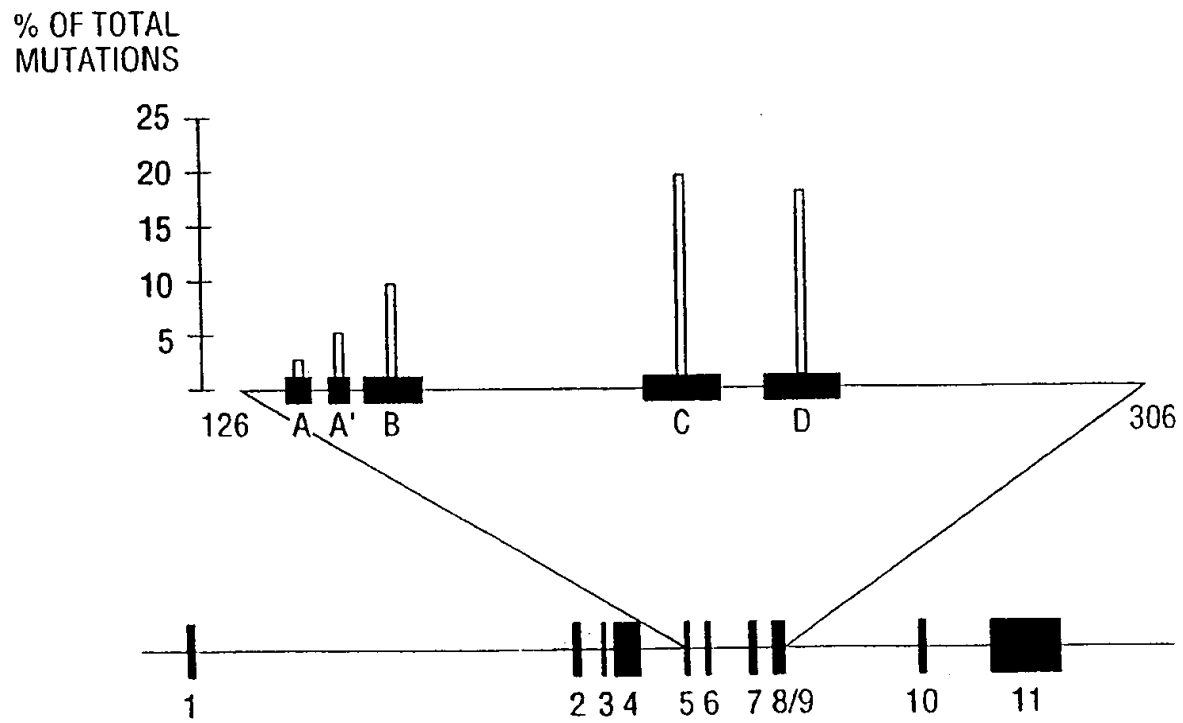


FIG. 76

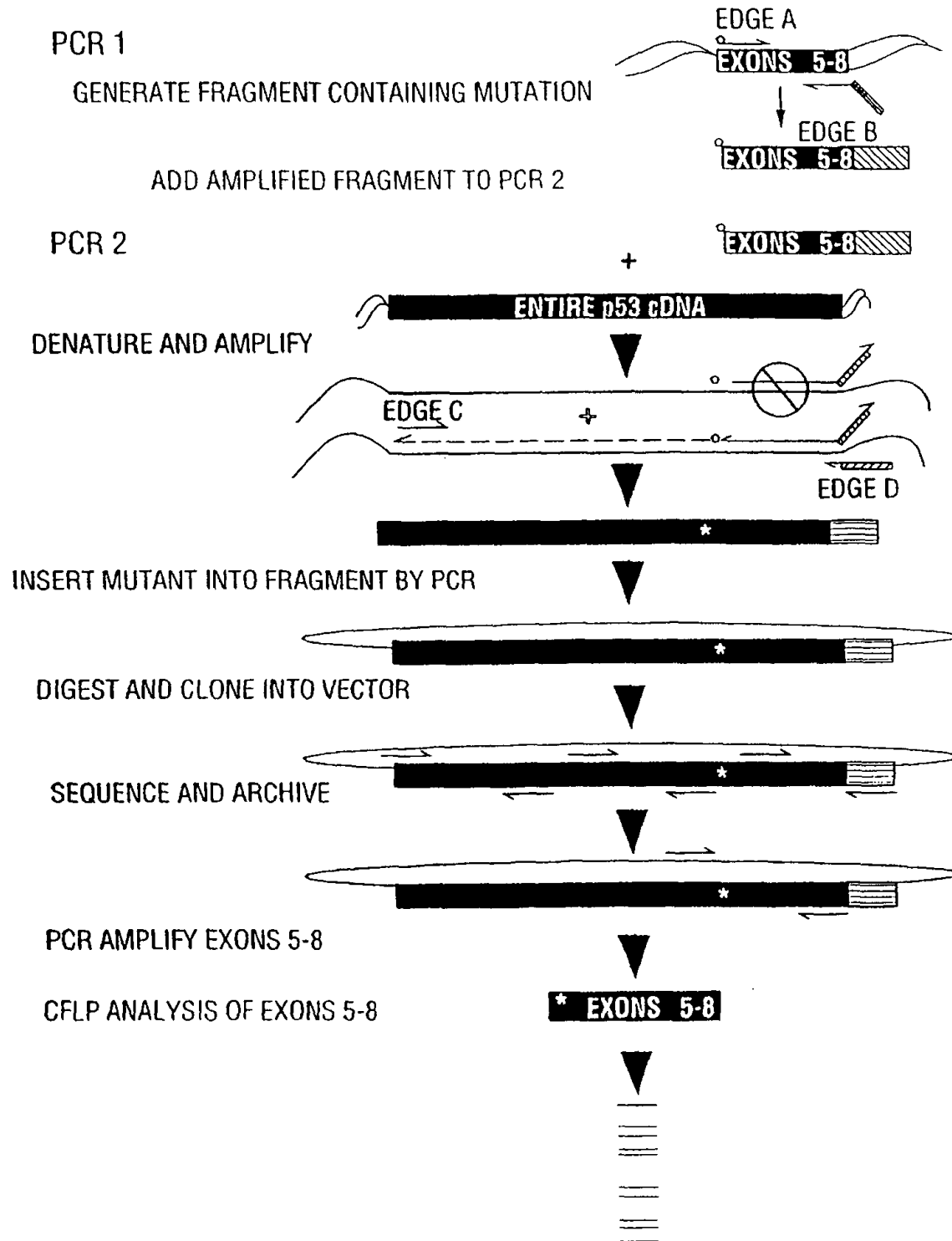


FIG. 77

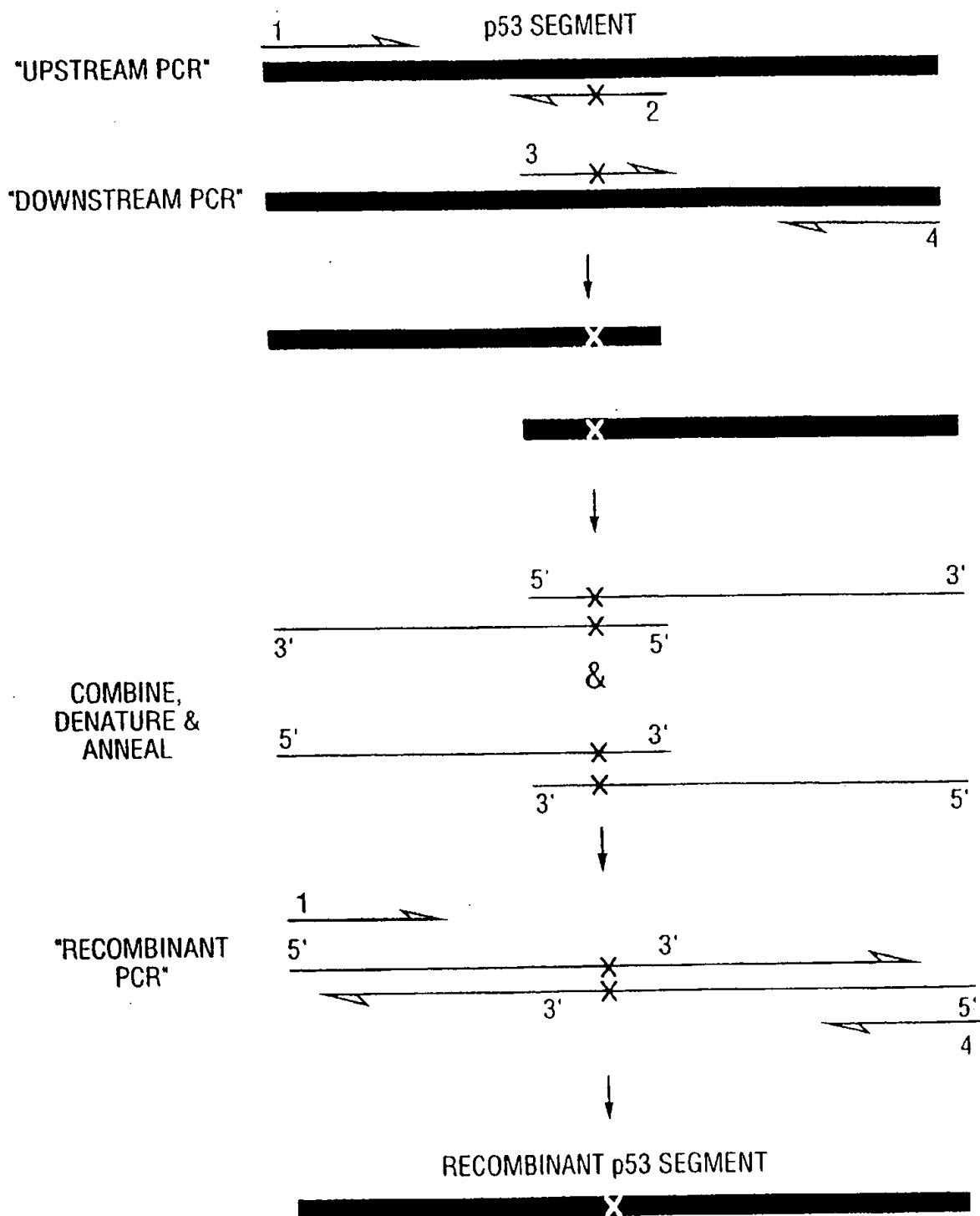


FIG. 78

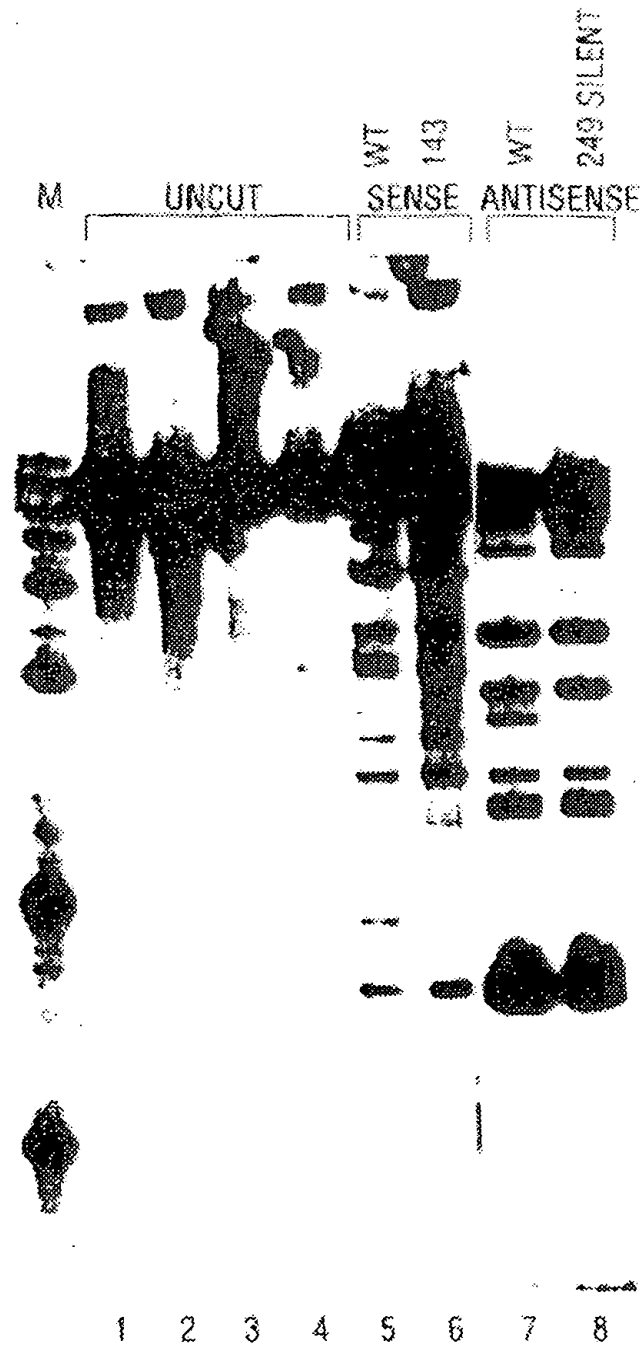


FIG. 79

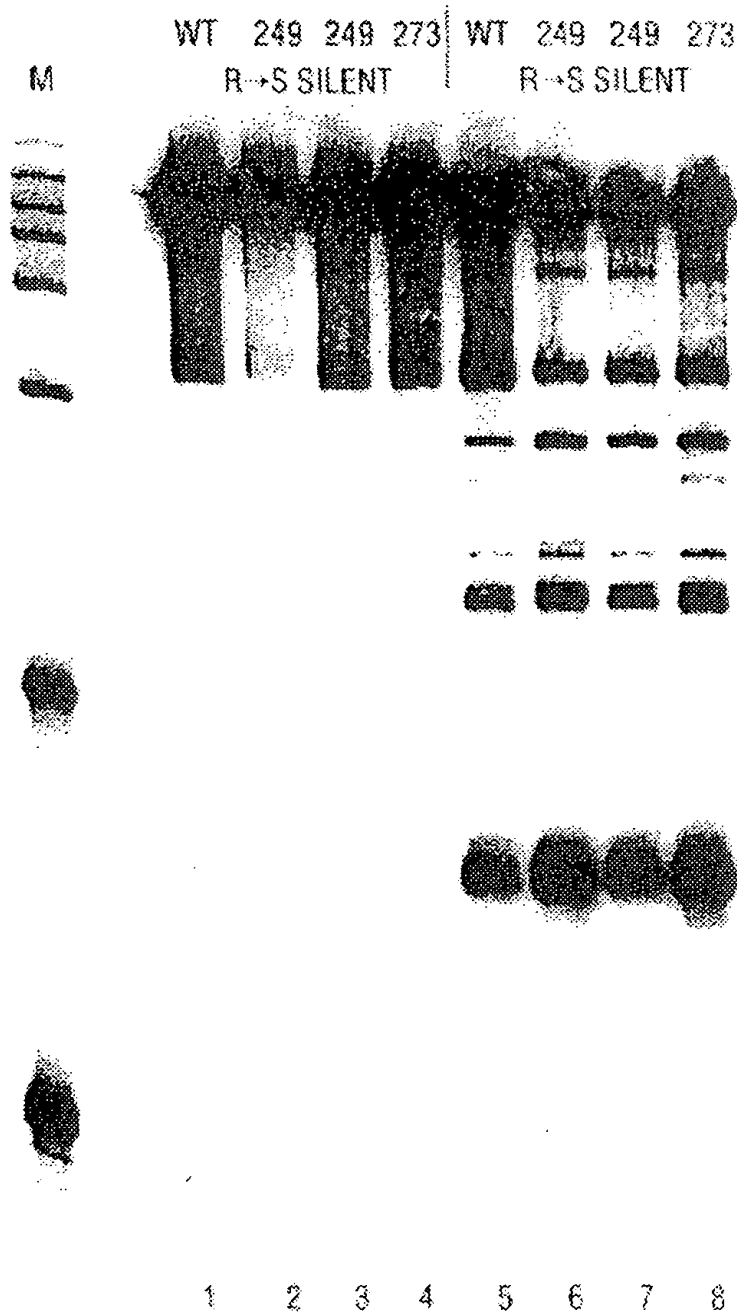


FIG. 80

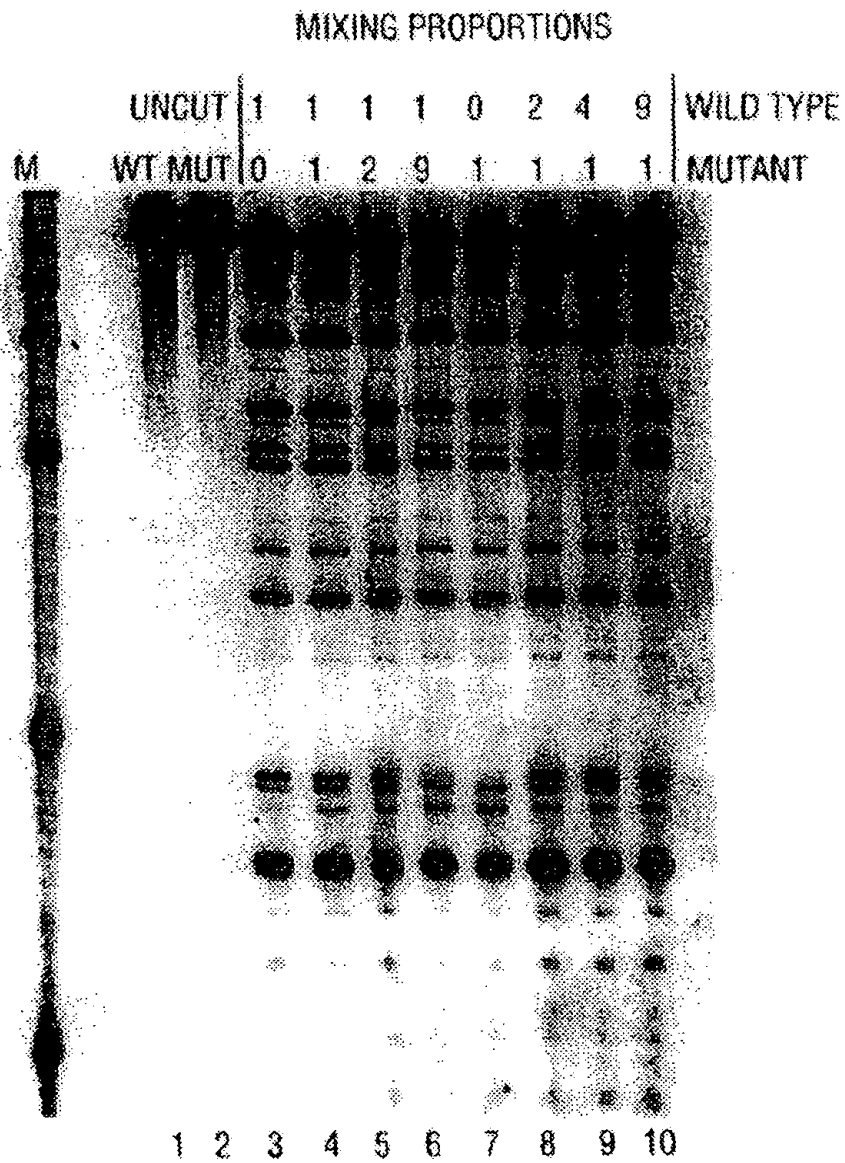


FIG. 81

HCV1.1	(SEQ ID NO:121)	1	CTGTCCTTCAC	GCAGAAAGCG	TCTGGCCATG	GCGTTAGTAT	GAGTGTCTGTG	50
HCV2.1	(SEQ ID NO:122)		CTGTCCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV3.1	(SEQ ID NO:123)		CTGTCCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV4.2	(SEQ ID NO:124)		CTGTCCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV6.1	(SEQ ID NO:125)		CTGTCCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV7.1	(SEQ ID NO:126)		CTGTCCTTCAC	GCAGAAAGCG	CTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV1.1		51	CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	100
HCV2.1			CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV3.1			CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV4.2			CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV6.1			CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV7.1			CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV1.1		101	GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT- <u>AAA</u>	150
HCV2.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-CAA	
HCV3.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-CAA	
HCV4.2			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	GGGATGIAA	
HCV6.1			GGTGAGTACA	CCGGAATTGC	CGGAAGACT	GGGTCCTTTC	TTGGAT- <u>AAA</u>	
HCV7.1			GGTGAGTACA	CCGGAATCGC	IGGGIGACC	GGGTCCTTTC	TTGGAG-CAA	

FIG. 82A

HCV1.1	151	CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	200
HCV2.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV3.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCGAGA	CTGCTAGCCG	
HCV4.2		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV6.1		CCCACTCIAT	GCCGGGCAAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV7.1		CCCGCTCAAT	ACCCAGAAAT	TTGGGCGTGC	CCCCGCGAGA	ICACTAGCCG	
HCV1.1	201	AGTAGTGTTG	GGTCGCCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	250
HCV2.1		AGTAGTGTTG	GGTCGCCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV3.1		AGTAGTGTTG	GGTCGCCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV4.2		AGTAGTGTTG	GGTCGCCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV6.1		AGTAGCGTTG	GGTIGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV7.1		AGTAGTGTTG	GGTCGCCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV1.1	251	GCGAGTGCCC	CGGAGGGTCT	CGTAGACCGT	GC	282	
HCV2.1		GCGAGTGCCC	CGGAGGGTCT	CGTAGACCGT	GC		
HCV3.1		GCGAGTGCCC	CGGAGGGTCT	CGTAGACCGT	GC		
HCV4.2		GCGAGTGCCC	CGGAGGGTCT	CGTAGACCGT	GC		
HCV6.1		GCGAGTACCC	CGGAGGGTCT	CGTAGACCGT	GC		
HCV7.1		GCGAGTGCCC	CGGAGGGTCT	CGTAGACCGT	GC		

FIG. 82B

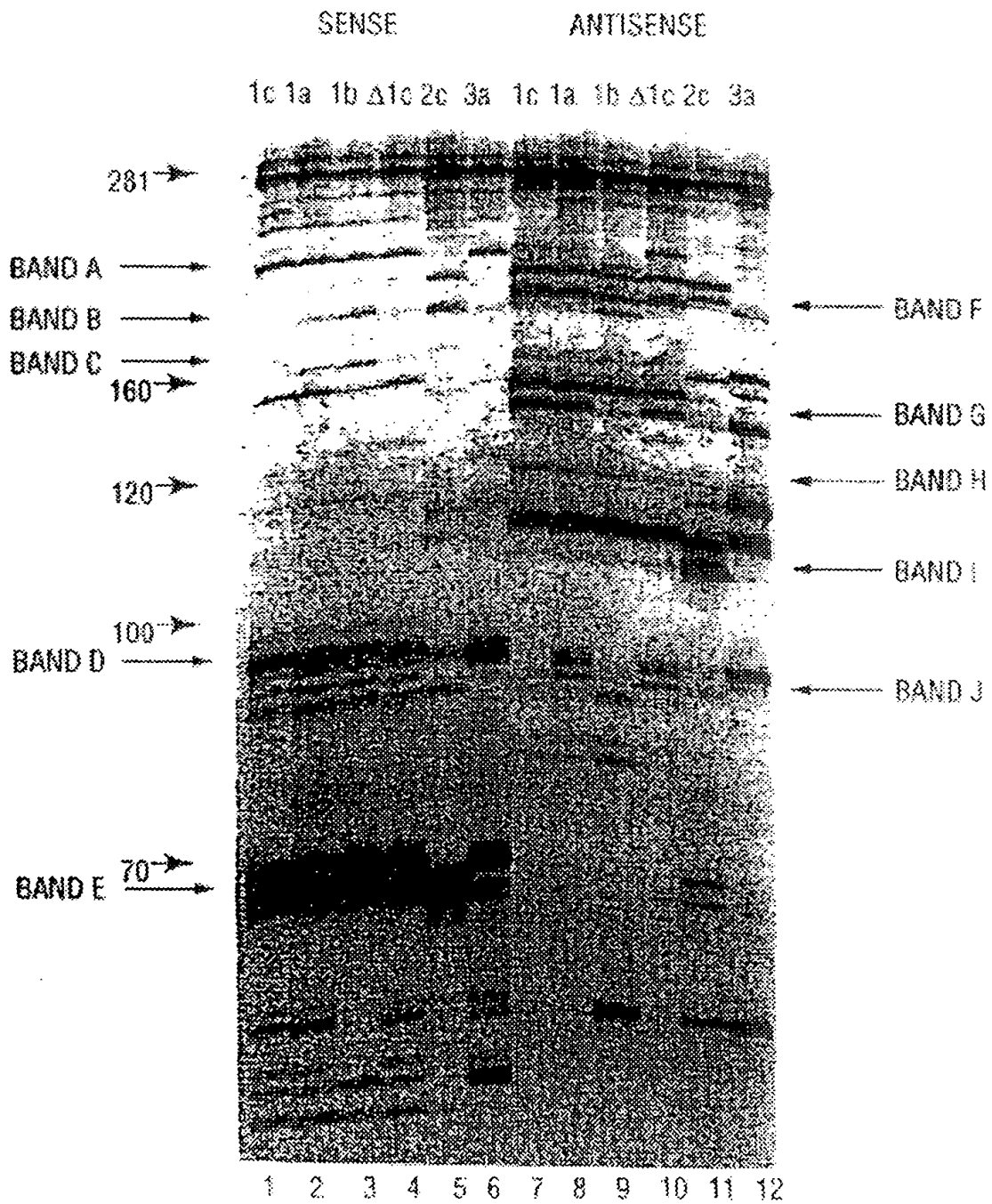


FIG. 83

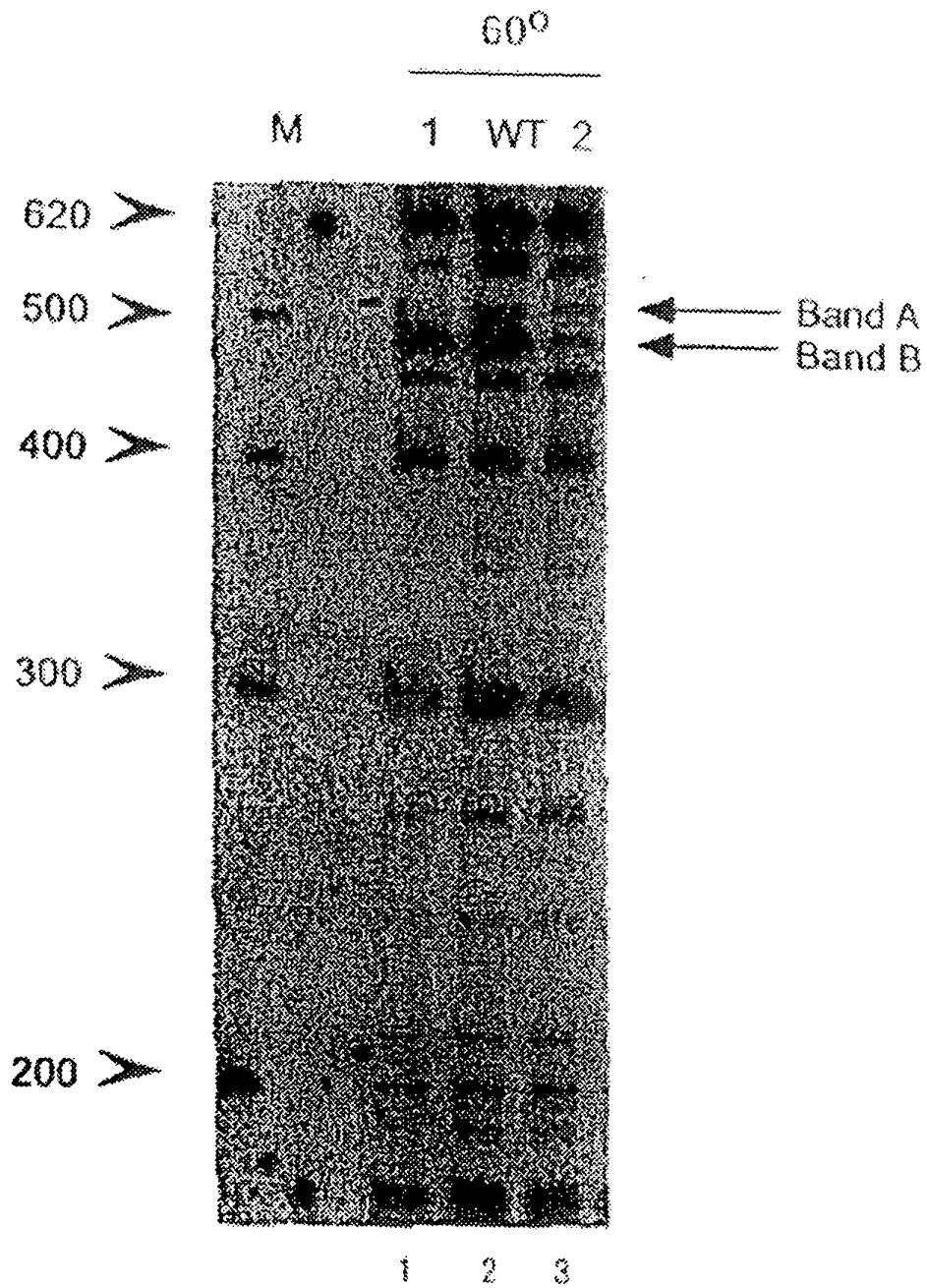


FIG. 84

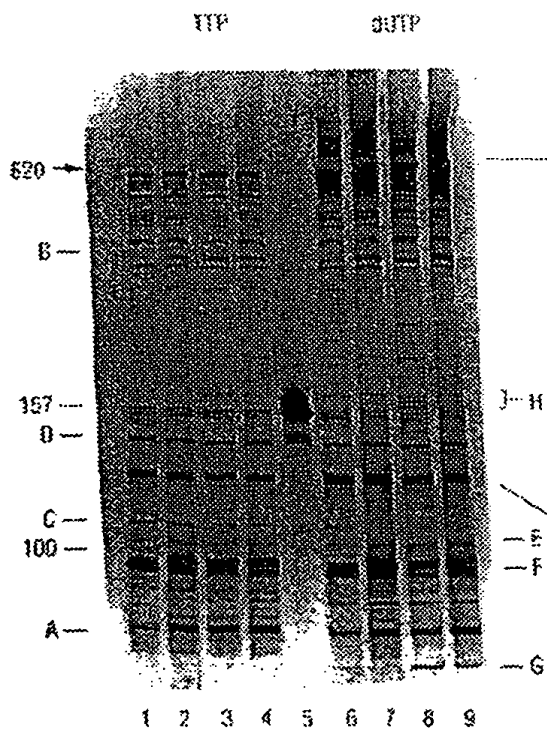


FIG. 85A

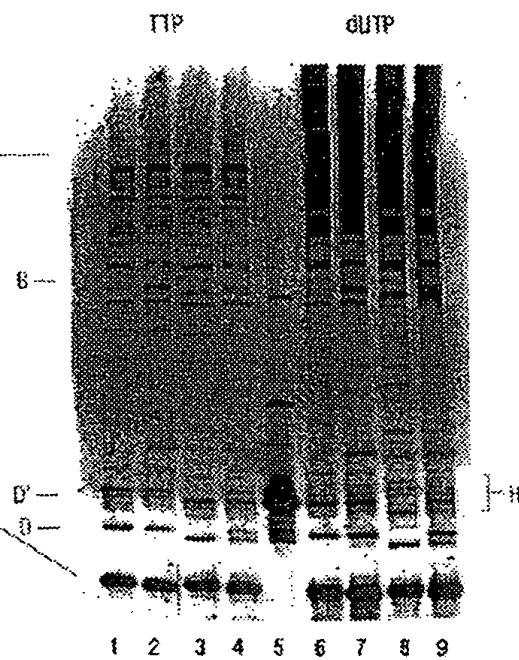


FIG. 85B

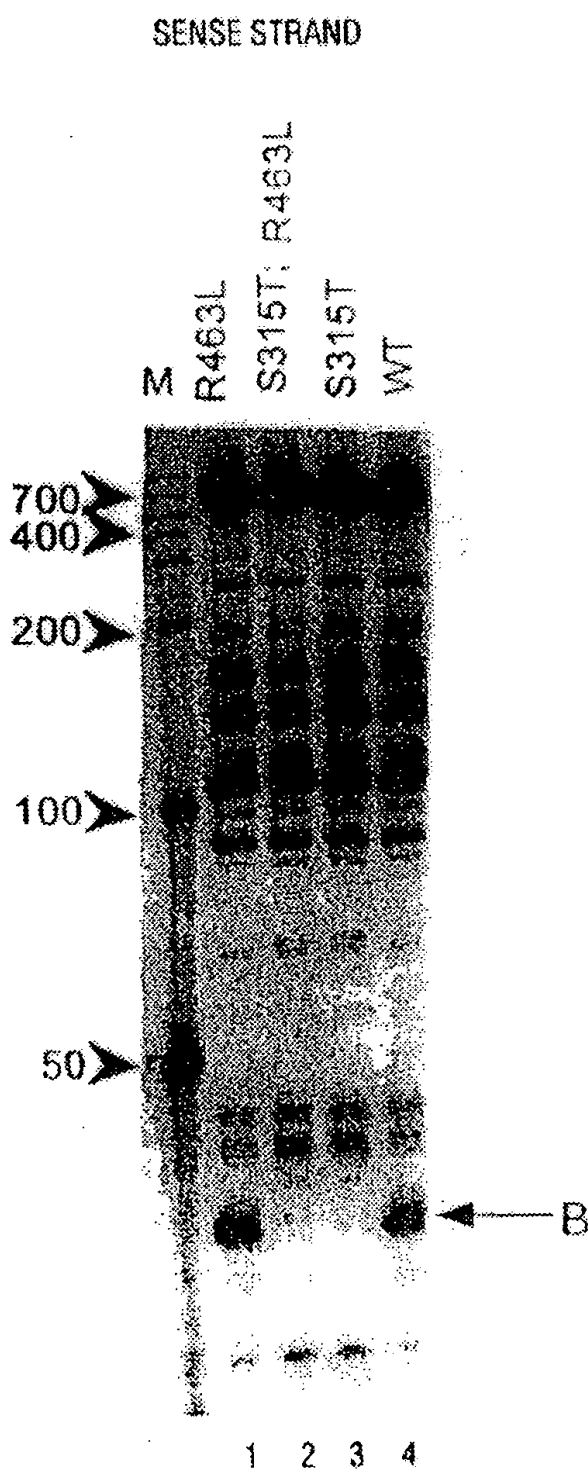


FIG. 86

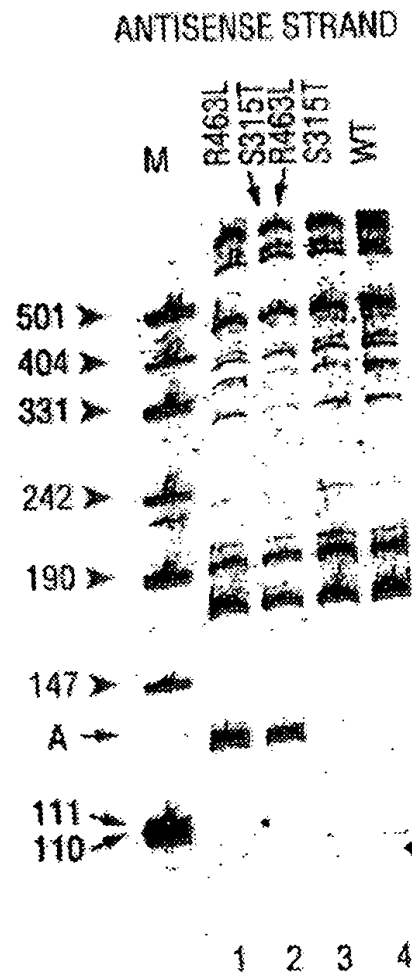


FIG. 87

1638

AGA GTTIGATCCT GGCTCAG
AAATTGAAGA GTTIGATCAT GGCICAGATT GAACGCTGGC GGCAGGCCTA ACACATGCAA
TTTAACCTCT CAAACTAGTA CCGAGTCTAA CTTGCGACCG CCGTCCGGAT TGTGTACGTT

1659

GGATGACCAAG CCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTGG
CCTACTGGTC GGTGTGACCT TGACTCTGTG CCAGGTCTGA GGATGCCCTC CGTCGTCACC
TGA GGATGCCCTC CGTCGTC

FIG. 88A

09940925 . 0222602

370	380	390	400	410	420
GGAATATTGC	ACAATGGGCG	CAAGCCTGAT	GCAGCCATGC	CGCGTGTATG	AAGAAGGCCT
CCTTATAACG	TGTTACCCGC	GTTCGGACTA	CGTCGGTACG	GGCACATAC	TTCTTCCGGA
430	440	450	460	470	480
TCGGGTTGTA	AAGTACTTTC	AGCGGGGAGG	AAGGGAGTAA	AGTTAATACC	TTTGCTCATT
AGCCCCAACAT	TTTCATGAAAG	TCGCCCCCTCC	TTCCCTCATT	TCAATTATGG	AAACGAGTAA
490	500	510	520	530	540
GACGTTACCC	GCAGAAGAAG	CACCGGCTAA	CTCCGTGCCA	GCAGCCGCGG	TAATACGGAG
CTGCAATGGG	CGTCTTCTTC	GTGGCCCGATT	GAGGCACGGT	CGTCGGCGCC	ATTATGCCTC
550	560	570	580	590	600
GGTGCAAGCG	TTAATCGGAA	TTACTGGGCG	TAAAGCGCAC	GCAGGCGGTT	TGTTAAGTCA
CCACGTTTCG	AATTAGCCTT	AATGACCCCG	ATTTCGCGTG	CGTCCGCCAA	ACAATTTCAGT
610	620	630	640	650	660
GATGTGAAAT	CCCCGGGCTC	AACCTGGGAA	CTGCACTCTGA	TACTGGCAAG	CTTGAGTCTC
CTACACTTTA	GGGGCCCGAG	TTGGACCCCTT	GACGTAGACT	ATGACCCGTT	GAACTCAGAG
670	680	690	700	710	720
GTAGAGGGGG	GTAGAATTCC	AGGTGTAGCG	GTGAAATGCG	TAGAGATCTC	GAGGAATACC
CATCTCCCCC	CATCTTAAGG	TCCACATCGC	CACTTTACGC	ATCTCTAGAC	CTCCTTATGG
730	740	750	760	770	780
GGTGGCGAAG	GCGGGCCCCCT	GGACGAAGAC	TGACGCTCAG	GTGCGAAAGC	GTGGGGAGCA
CCACCGCTTC	CGCCGGGGGA	CCTGCTTCTG	ACTGCGAGTC	CACGCTTTCG	CACCCCTCGT

FIG. 88B

1210	1220	1230	1240	1250	1260	
ATCATGGCCC TTA						SB-3
ATCATGGCCC TTACGA						SB-4
ATCATGGCCC TTACGACCAG	GGCTACACAC	GTGCTACAAT	GGCGCATACA	AAGAGAAAGCG		
TAGTACCGGG AATGCTGGTC	CCGATGTGTG	CACGATGTTA	CCGCGTATGT	TTCTCTTCGC		
1270	1280	1290	1300	1310	1320	
ACCTCGCGAG AGCAAGCGGA	CCTCATAAAG	TCCGTCGTAG	TCCGGATTGG	AGTCTGCAAC		
TGGAGCGGCTC TCGTTCGCCT	GGAGTATTTC	ACGCAGCATC	AGGCCTAACC	TCAGACGTTG		
1330	1340	1350	1360	1370	1380	
TCGACTCCAT GAAGTCGGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATACGT		
AGCTGAGGTA CTTCAGCCTT	AGCGATCATT	AGCACCTAGT	CTTACGGTGC	<u>CACTTAIGCA</u>		
			GC	CACTTATGCA		1743
1390	1400	1410	1420	1430	1440	
TCCCGGGCCT TGTACACACC	GCCCCGTCACA	CCATGGGAGT	GGGTTGCAAA	AGAAAGTAGGT		
AGGGCCCCGGA ACAIGTGTGG	CGGGCAGTGT	GGTACCCTCA	CCCAACGTTT	TCTTCATCCA		
AGGGCCCCGGA ACATG						1743
1450	1460	1470	1480	1490	1500	
AGCTTAACCT TCGGGAGGGC	GCTTACCACT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA		
TCGAATTGGA AGCCCTCCCG	CGAATGGTGA	AACACTAAGT	ACTGACCCCA	CTTCAGCATT		
1510	1520	1530	1540	1550		
CAAGGTAACC GTAGGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA.....			
GTTCCATTGG CATCCCCCTG	GACGCCAACC	TAGTGGAGGA	AT.....			

FIG. 88D

1638 (SEQ ID NO:151)	AGAGTTTGATCCTGGCTCAG
E.colirrsE(SEQ ID NO:158)0	...AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGACGGCTTAACACATGCA
Cam.jejun5(SEQ ID NO:159)0	~TTTTATGGAGAGTTTGATCCTGGCTCAGAGTGAACGCTGGCGGCTGCTTAATACATGCA
Stp.aureus(SEQ ID NO:160)0	. .TTTTATGGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCTGCTTAATACATGCA
ER10 (SEQ ID NO:152)	
E.colirrsE	60 AGTCGAACGGTAACAG----GAAGAAAGCTTGCTTCTTT----GCTGACGAGTGGCGGACGGG
Cam.jejun5	62 AGTCGAACGAT-----GAAGCTTCTAGCTTGCTAGAAAGTGA-----TTAGTGGCGCACGGG
Stp.aureus	61 AGTCGAGCGAA-----CGGACGAGAAAGCTTGCTTCTCTGATG----TT-AGCGGCGGACGGG
ER10	TGAGTAA
E.colirrsE	114 TGAGTAATGTCTGGGA-AACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATA
Cam.jejun5	114 TGAGTAAGGTATAGTTAATCTGCCCTACACAAGAGGACAAACAGTTGGAAACGACTGCTAATA
Stp.aureus	113 TGAGTAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCTAATA
E.colirrsE	175 CCGCATAAC-----GTCGCAAGAC-----CAAAGAGGGGACCTTCG-GGCCTCTTG
Cam.jejun5	176 CTCTATACTCCTGCTTAACACAAAGTTGAGTAGG-GAAAG-----TTTTT-----CG
Stp.aureus	175 CCGGATAATATTTGAACCGCATGTTCAAAAGTGAAAGACGGT----CTT----GCTGTCA
E.colirrsE	221 CCATCGGATGTGCCAGATGGGATTAGCTAGTAGTGGGTAAACGGCTCACCTAGGCGACGA
Cam.jejun5	221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGGTAAATGGCTTACCAAGGCTATGA
Stp.aureus	229 CTTATAGATGGATCCGCGCTGCATTAGCTAGTTGGTAAGGTAAACGGCTTACCAAGGCAACGA
E.colirrsE	283 TCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTA
Cam.jejun5	283 CGCTTAACCTGGTCTGAGAGGATGATCAGTCACACTGGAACCTGAGACACGGTCCAGACTCCTA
Stp.aureus	291 TACGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACACGGTCCAGACTCCTA
1659 (COMPL)	ACTCCTA

FIG. 89A

E.colirrsE	345	CGGGAGGCAGCAGTGGGGAATATTGCACAAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTG
Cam.jejun5	345	CGGGAGGCAGCAGTAGGGAATATTGCGCAATGGGGAAACCTTGACGCAGCAACGCCGCGTG
Stp.aureus	353	CGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTG
1659 (COMPL)		CGGGAGGCAGCAG
E.colirrsE	407	TATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTTCAGCGGGAGGAA-GGGAGTAAAGTTAAT
Cam.jejun5	407	GAGGATGACACTTTTCGGAGCGTAAACTCTTTTCTTAGGGAAG -----AATT
Stp.aureus	415	AGTGATGAAGGTCTTCGGATCGTAAACTCTGTTATTAGGGAAGACATATGTGTAAAGTAAC
E.colirrsE	468	ACCTTTGCTCATTGACGTTACCCGCGAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCG
Cam.jejun5	455	C-----TGACGGTACCTAAGGAATAAGCACCGGCTAACTCCGTGCCAGCAGCCGCG
Stp.aureus	476	-TGTCACATCTTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCG

FIG. 89B

E.colirrsE	840	C-CTTGA-GGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGC
Cam.jejun5	816	G-CTAGT-CATCTCAGTAATGCAGCTAACGCCATTAAAGTGTAACCGCTGGGAGTACGGTCGC
Stp.aureus	848	GT-TTCCGCCCTTAGTGCTGCAGCTAACGCATTAAAGCACTCCGCCTGGGGAGTACGACCGC
E.colirrsE	900	AAGGTTAAAACTCAAATGAATTGACGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAATT
Cam.jejun5	876	AAGATTAAAACTCAAAGGAATAGACGGGGACCCGCAACGCGGTGGAGCATGTGGTTTAATT
Stp.aureus	909	AAGGTTGAAACTCAAAGGAATTGACGGGGACCCGCAACGCGGTGGAGCATGTGGTTTAATT
E.colirrsE	962	CGATGCAACGCGAAGAACCTTACCTGGTCTTTGACATCCACGGAAGTTTTTCAGAGATGAGAAT
Cam.jejun5	938	CGAAGATACGCGAAGAACCTTACCTGGGCTTGATATCCTAAGAAACCTTTTAGAGATAAGAGG
Stp.aureus	971	CGAAGCAACGCGAAGAACCTTACCAAATCTTGACATCCTTTGACAACTCTAGAGATAGAGCC
E.colirrsE	1024	GTG--CCTTCGGG--AA-CCGTGAGACAGGTGCTGCATGGCTGTCAGCTCGTGTGTGA
Cam.jejun5	1000	GTGCTAGCTTTGCTAGAA-CTTAGAGACAGGTGCTGCACGGCTGTCGTAGCTCGTGTGTGA
Stp.aureus	1033	TTCC-CCTTCGGG--GGACAAAGTGACAGGTGGTGCAATGGTTGTCGTAGCTCGTGTGTGA
SB-1		GCAACGAGCGCAACCC
E.colirrsE	1081	AATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTATCCTTTGTTGCCAGCGGTCCGG-CC
Cam.jejun5	1061	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCACGTAATTTAGTTGCTAACGGTTCGG-CC
Stp.aureus	1092	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTAAGCTTAGTTGCCATCA-TTAAGT-T

FIG. 89D

SB-3 (SEQ ID NO: 157)	ATGACGTC	CAAGTCATC		
SB-4 (SEQ ID NO: 154)	ATGACGTC	CAAGTCATC		
E.colirrsE	1142	GGGAAC	TCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTC	CAAGTCATC
Cam.jejun5	1122	GAGCACTCTAAATAGACTGCCCTTCG-TAAGGAGGAGGAAGGTGTGGACGACGTC	CAAGTCATC	
Stp.aureus	1152	GGGCAC	TCTAAGTTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTC	CAAATCATC
SB-3		ATGGCCCTTA		
SB-4		ATGGCCCTTACGA		
E.colirrsE	1204	ATGGCCCTTACGACCAAGGCTACACACGTGCTACAAATGGCGCATACAAAGAGAGCGACCTC		
Cam.jejun5	1183	ATGGCCCTTATGCCCAGGCGACACACGTGCTACAAATGGCATATAGAAATGAGACGCAATACC		
Stp.aureus	1214	ATGCCCTTATGATTTGGGCTACACACGTGCTACAAATGGACAAATACAAAGGCGAGCGAAACC		
E.colirrsE	1266	GCAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTC		
Cam.jejun5	1245	GCAGGTGGAG-CAAAATCTATAAAATATGTCCCAGTTCGGATTGTTCTCTGCAACTCGAGAG		
Stp.aureus	1276	GCAGGTCAAGCAAAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTA		
E.colirrsE	1328	CATGAAGTCGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATACGTTCCCGGGC		
Cam.jejun5	1306	CATGAAGCCGGAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCGGGT		
Stp.aureus	1338	CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCGGGT		
1743(compl)		CGGTGAATACGTTCCCGGGC		

FIG. 89E

E.colirrsE	1389	CTTG	TACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAGTAGGTTAACCT
Cam.jejun5	1368	CTTG	TACTCACC GCCCGTCACACCATGGGAGTTGATTTCACTCGAAGCCGGAATACT--A-A
Stp.aureus	1399	ATTG	TACACACCGCCCGTCACACACCGAGAGTTTGTAAACACCCGAGCCGGTGAGTAACCT
1743 (compl)		CTTG	TAC
E.colirrsE	1451	TCG	_GGAGGGCGCTTACCACCTTTGTGATTCATGACTGGGGTGAAGTCGTAACAAGGTAACCG
Cam.jejun5	1427	AC	--T-AGTTACCGTCCACAGTGGAATCAGCGACTGGGGTGAAGTCGTAACAAGGTAACCG
Stp.aureus	1461	TTTAGGAGCTAGCCGTCGAAGGTGGGACAAATGATTGGGGTGAAGTCGTAACAAGGTAGCCG	
E.colirrsE	1512	TAGGGGAACCTGCGGGTTGGATCACCTCCTTA---	
Cam.jejun5	1485	TAGGAGAACCTGCGGGTTGGATCACCTCCT-----	
Stp.aureus	1523	TATCGGAAGGTGCGGCTGGATCACCTCCTTTCT-	

FIG. 89F

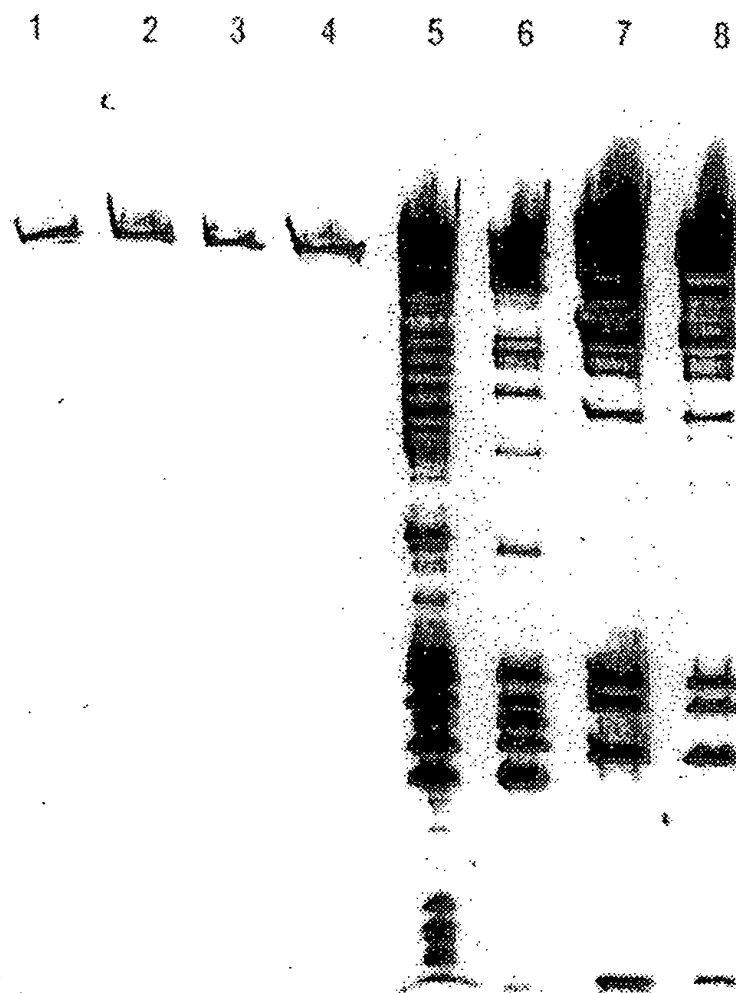


FIG. 90

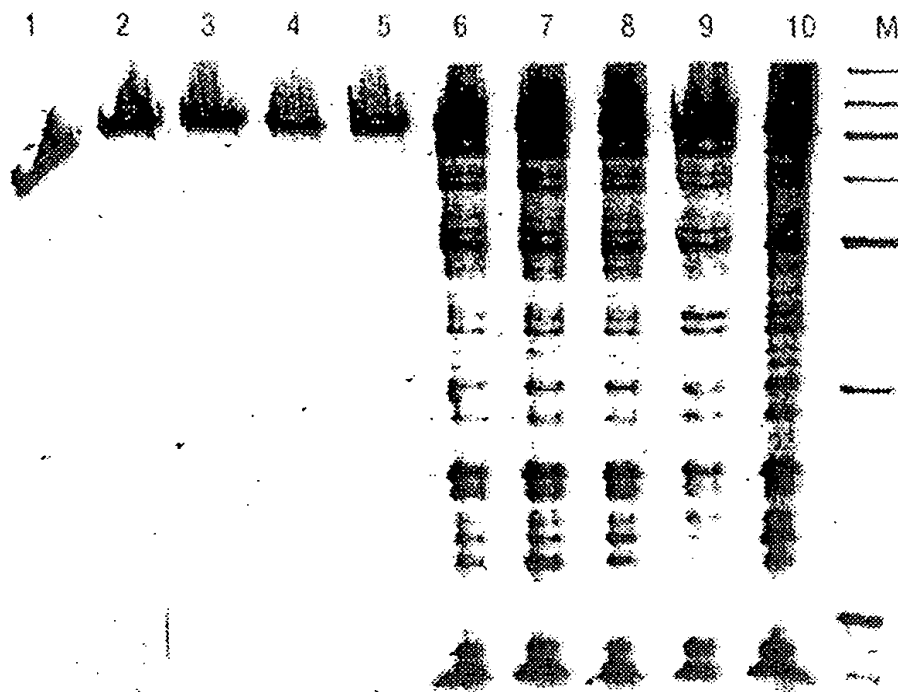


FIG. 91A

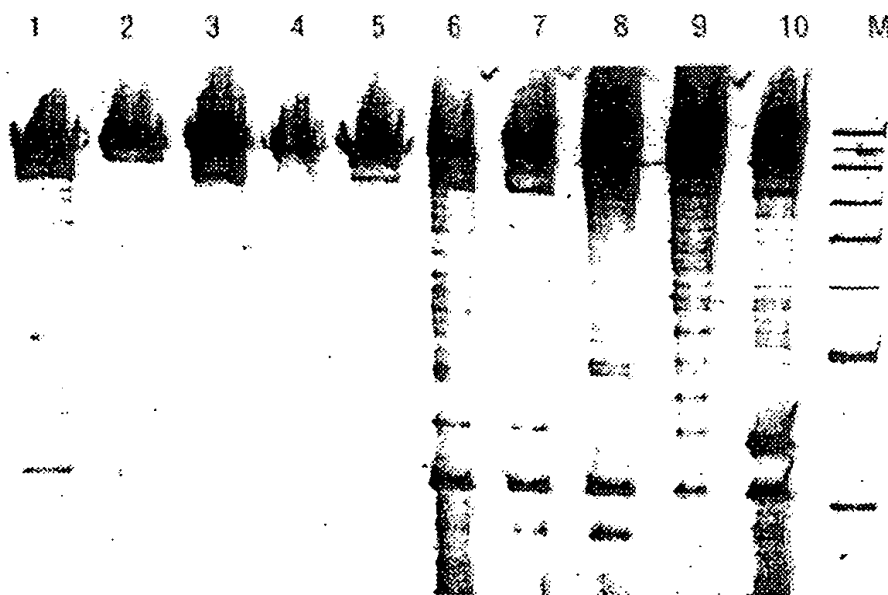
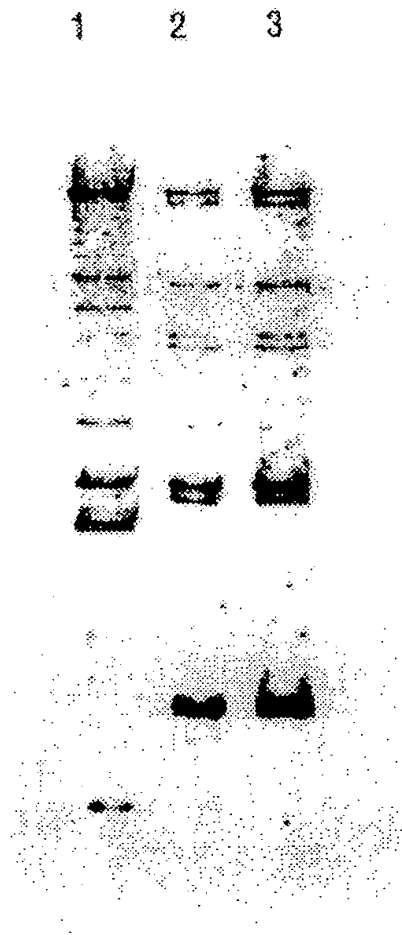


FIG. 91B

**FIG. 92**

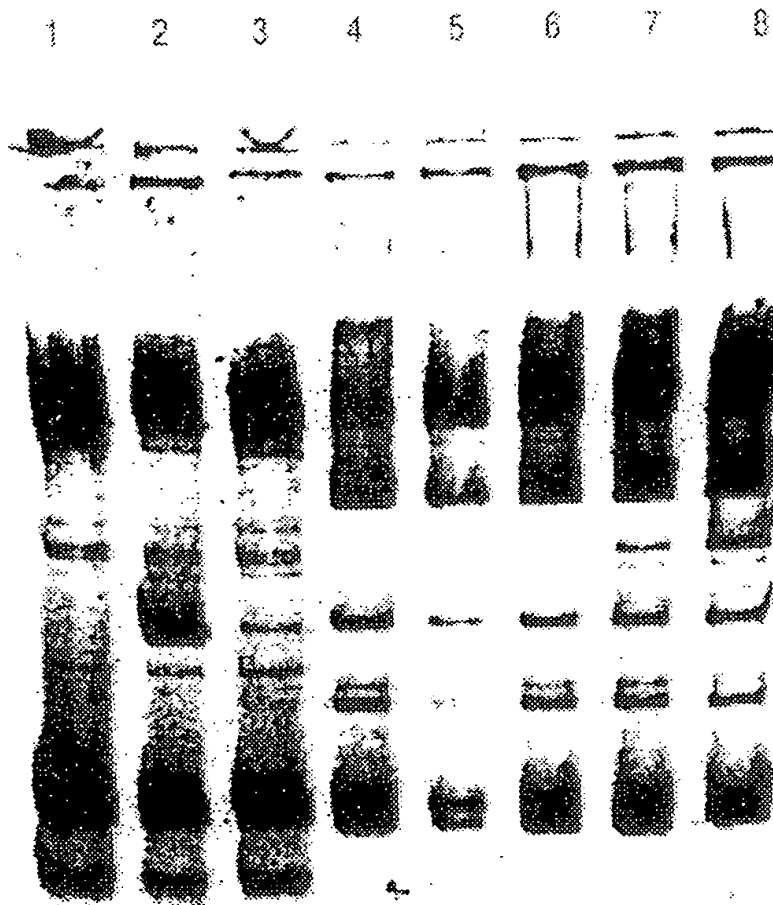


FIG. 93

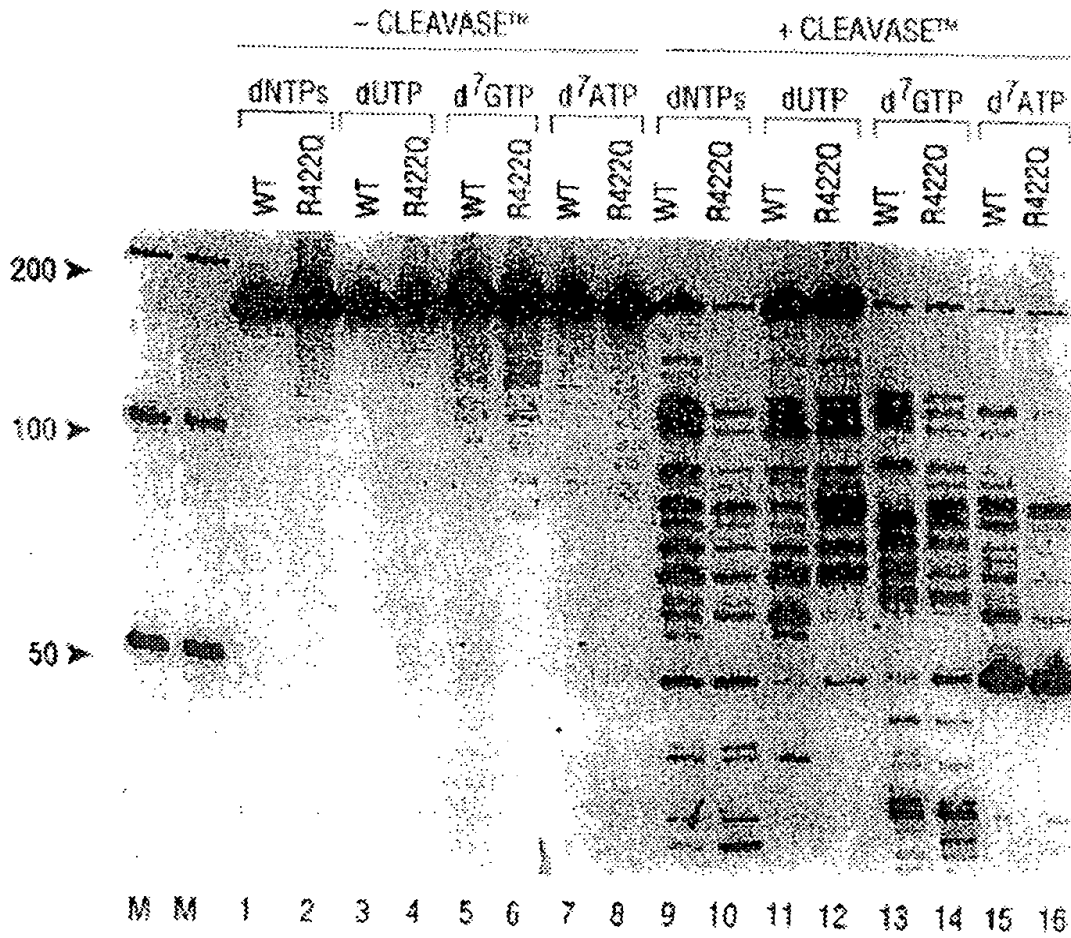


FIG. 94